

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 26.813 Seconds
(without alignments)
1008.352 Million cell updates/sec

Title: US-10-662-429-2
Perfect score: 1478
Sequence: 1 MAMMEVQGSPSLGTCVTLV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189.5	12.8	279	2 A53062	Fas ligand - mouse
2	186	12.6	281	2 I38707	Fas ligand - human
3	177.5	12.0	278	2 A49266	fas ligand - rat
4	164	11.1	261	2 S53090	CD40 ligand - bovi
5	147.5	10.0	261	2 I53476	CD40 ligand - huma
6	141	9.5	234	1 A25451	tumor necrosis fac
7	141	9.5	260	2 S21738	CD40 ligand - mous
8	134.5	9.1	204	1 S17289	tumor necrosis fac
9	133	9.0	232	1 S12606	tumor necrosis fac
10	131.5	8.9	233	1 S22052	tumor necrosis fac
11	131	8.9	234	1 J01344	tumor necrosis fac
12	130.5	8.8	233	1 S24642	tumor necrosis fac
13	129.5	8.8	235	2 S54490	tumor necrosis fac
14	127.5	8.6	204	1 S24641	lymphotoxin - bovi
15	125.5	8.5	233	1 QWHUN	tumor necrosis fac
16	123.5	8.4	235	1 QMNSN	tumor necrosis fac
17	123.5	8.4	235	2 JU0029	tumor necrosis fac
18	122	8.3	205	1 QHUXH	lymphotoxin alpha
19	121	8.2	234	1 JH0529	tumor necrosis fac
20	115.5	7.8	193	2 S06192	tumor necrosis fac
21	114	7.7	202	1 B27303	tumor necrosis fac
22	113.5	7.7	185	2 S52715	tumor necrosis fac
23	113.5	7.7	306	2 I49139	lymphotoxin-beta -
24	112.5	7.6	638	1 QOBY2M	mRNA maturation bi4
25	111.5	7.5	202	1 JN0869	tumor necrosis fac
26	109	7.4	652	2 I48083	amphotropic murine
27	107	7.2	197	1 JH0309	tumor necrosis fac
28	102	6.9	244	2 A46066	lymphotoxin beta -
29	100	6.8	865	2 AB1658	probable membrane

30 99.5 6.7 233 2 S11688 tumor necrosis fac
31 97.5 6.6 448 2 F95122 protein kinase, pr
32 95 6.4 345 2 T14707 DNA ligase homolog
33 95 6.4 365 2 T15010 hypothetical prote
34 95 6.4 455 2 G95104 hypothetical prote
35 94.5 6.4 4981 2 T18489 hypothetical prote
36 94 6.4 1465 2 T23056 chromodomain helic
37 92.5 6.3 833 1 A31593 heat shock transcr
38 92.5 6.3 1538 2 T29095 cardiac muscle fac
39 91 6.2 1176 2 JN0583 myosin-light-chain
40 90.5 6.1 502 2 JC2491 serine/threonine k
41 90.5 6.1 502 2 A53444 activin receptor-1
42 90.5 6.1 1284 2 T40578 hypothetical prote
43 90 6.1 907 2 E96636 hypothetical prote
44 89.5 6.1 313 2 T03031 NBS-LRR type resis
45 89 6.0 328 2 B59296 alpha-N-arabinotur

ALIGNMENTS

RESULT 1

A53062
Fas ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A53062
R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A;Reference number: A53062; MUID:94185175; PMID:7511063
A;Accession: A53062
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-279 <TAK>
A;Cross-references: UNIPROT:P41047; GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match 12.8%; Score 189.5; DB 2; Length 279;

Best Local Similarity 25.8%; Pred. No. 1.7e-08;

Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

Qy 83 QLRLVRKMLTSLSEETISTVQEKQNIPLVRRGQORVAAHITGTRGRSNTLSSPNSK 142
Db 111 ELREFTKQSL-----KVSSFQKIAMPSTPEKKEPRSV-AHUTG-----NPHSR 154
Qy 143 NEKALGRKINSWSSRSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKN 202
Db 155 SIPL-----EWEDT-YGTALISGVKYKGGVLINETGLYFVYSKVYFRGQ-----SCN 201
Qy 203 DKQMVQVIY-KYTSYDPDILLMKAR-NSCWSKDAEYGLYSIYOGGIFELKENDRIFVSV 260
Db 202 NQPLNHKVYMRNSKYPEDLVMBEKLNYCTT--GQIWAHSSYLGAVENTLSADHLVYNI 259
Qy 261 TNEHLIDMDHEASFGAF 278
Db 260 SQLSLINFESKTFFGDLY 277

RESULT 2

I38707
Fas ligand - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38707; JC2340; S57565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.
A;Reference number: I38707; MUID:95127560; PMID:7826947
A;Accession: I38707
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RES>
A;Cross-references: UNIPROT:P48023; EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g59544

R;Mita, E.; Hayaashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: GB:D38122; DDBJ:D29820; NID:G601892; PIDN:BAA07320.1; PID:gi369902
R;Schatzlein, C.B.
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: EMBL:X89102; NID:G887455; PID:G887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:G624627; PIDN:AAC50071.1; PID:G624628
C;Genetic: FasL
A;Gene: FasL
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 186; DB 2; Length 281;
Best Local Similarity 22.1%; Pred. No. 3 4e-08;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

QY 4 MEVQGPSLGQTCVLIVFTVLQSLCAV---TYVYFTNELKQMDKYKSGIACFLKE 60
DB 71 LKRGHNSGTG-LCLLVWFVFLVALVGLGLGMPQLFHLQKELAELESTSQMHTASLEK 129
QY 61 DDSYNDPDEESMNSQWQVQWQLRQVLRKMLRTSEETISTVQEQQNISPLVRERGQ 120
DB 130 QIGHPSPPPE-----KKELRKV----- 146
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVTHEKG 180
DB 147 ---AHLT---GKSNRSMP-----LEWDT-VGIVLLSGVYKKGGLVINETG 187
QY 181 FYVIYSQTYFRFOEIKENTKNDKQMVQYIY-KYTSYDPDILLMKSGARNS-----CWSK 233
DB 188 LYPVYSKVYFRGQ-----SCNNLPLSHKYMYRNSKYPODLVNMEGKQMSYCTTGQMWAR 241
QY 234 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFCAP 278
DB 242 -----SSYLGAVFNLTSADHLVNVNSELVNFVESOTFFGLY 279

RESULT 3
A49266
fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor gene family.
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
A;Cross-references: UNIPROT:P36940; GB:U03470; NID:G440178; PIDN:AAC52129.1; PID:G440179
C;Keywords: glycoprotein; transmembrane protein

Query Match 12.0%; Score 177.5; DB 2; Length 278;
Best Local Similarity 27.5%; Pred. No. 1.8e-07;
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

QY 100 ISTVQEQQNISPLVREROPQVAAHITGT-RGRSNTLSSPNSKNEKALGRKINSWESSR 158
DB 121 VGSFEKQIANPSTPSETKKPRSV-AHLTGNPRSRSLP-----EWEDT- 162
QY 159 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIY-KYTSYP 217
DB 163 YGTALISGVYKKGGLVINEAGLYFYVKYFRGQ-----SCNSQPLSHKVMRNFKYP 216
QY 218 DPILLMKSR-NSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
DB 217 GDLVLMEEKKLVNCTI--CQIWAHSSYLGAVFNLTVDHLYVNISQLSINPEESKTFEG 274
QY 277 AF 278
DB 275 LY 276

RESULT 4
S53090
CD40 ligand - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S53090
R;Wentens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
A;Accession: S53090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <MER>
A;Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:G732569; PIDN:CAA88363.1; PID:G73255

Query Match 11.1%; Score 164; DB 2; Length 261;
Best Local Similarity 25.9%; Pred. No. 2.3e-06;
Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;

QY 6 VGGPSLGQTCVLIVFTVLL--QSLCAVAVYVYFTNELKQMDKYKSGIACFLKEDDS 63
DB 13 VATGPPVSMK-IFMYLLTVFLITQIMIGSALFAVYLHRRLDKIEDERLNHEDFVFMK--T 68
QY 64 YNDPNDDESMNS--PCWQVQWQLRQVLRKMLRTSEETISTVQEQQNISPLVRERGQ 121
DB 69 IQRCKNGEGSLNLLNCEEIRSRPEDLV-KDINQNK-----VKKKEKFMHKGQDFPQ- 121
QY 122 VAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHE 178
DB 122 IAAHV-----ISEASSKTSVL-----QW--APKGYITLSNNLVLTLENGKQLAVKR 165
QY 179 KGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDILLMKSGARNSCWSKDAEY 238
DB 166 QGFYIYITQVTFCSNRE---TLQAFFIASLCLKSPSGSERILLRAANTHSSSKFC--G 219
QY 239 LYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
DB 220 QOSIHLGGVFELOSGASVFVNVTDPSPQVSHGTGFTSFG 257

RESULT 5
I53476
CD40 ligand - human
N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: S28017; JH0793; S28852; S28694; S28582; S25684; S30593
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; Emswiler, J. J. Biol. Chem. 267, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for

A;Reference number: S28017; MUID:93049181; PMID:1385114

A;Accession: S28017

A;Molecule type: mRNA

A;Residues: 1-261 <HOL>

A;Cross-references: UNIPROT:P29965; EMBL:Z15017; NID:G38483; PIDN:CAA78737.1; PID:G38484

R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.

J. Exp. Med. 176, 1543-1550, 1992

A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin

A;Reference number: JH0793; MUID:93094757; PMID:1281209

A;Accession: JH0793

A;Molecule type: mRNA

A;Residues: 1-261 <SPR>

A;Cross-references: GB:X67878; NID:G38411; PIDN:CAA48077.1; PID:G38412

A;Experimental source: peripheral blood T-cell

R;Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroczeck, R.A.

Eur. J. Immunol. 22, 3191-3194, 1992

A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.

A;Reference number: S26694; MUID:93076854; PMID:1280226

A;Accession: S26694

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-261 <GRA>

A;Cross-references: EMBL:X68550; NID:G37269; PIDN:CAA48554.1; PID:G37270

R;Gauchat, J.P.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.

FEBS Lett. 315, 259-266, 1993

A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e

A;Reference number: S28852; MUID:93138085; PMID:7678552

A;Accession: S28852

A;Molecule type: mRNA

A;Residues: 1-261 <GAU>

A;Cross-references: EMBL:L07414; NID:G180123; PIDN:AAA35662.1; PID:G180124

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln

C;Genetics:

A;Gene: GDB:CD40LG; HIGM1; IMD3

A;Cross-references: GDB:120632; OMIM:308230

A;Map position: Xq26-Xq26

C;Keywords: glycoprotein; transmembrane protein

F;13-44/Domain: transmembrane #status predicted <TM>

F;45-261/Domain: extracellular #status predicted <EXT>

F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 10.0%; Score 147.5; DB 5; Length 261;

Matches 66; Conservative 51; Mismatches 99; Indels 63; Gaps 15;

QY 17 VLIVFTVLL--QSLCAVAVYVFTNELKQMDKQKSGIACFLKEDDSYNDP-----ND 69

DB 23 IFMYLLTVLITQWISALFAVYLHRLDKIEDERN-----LHEDFVFMKTIQRCNTG 75

QY 70 EESNN-SPCQVQKQLRQLVRKMLRTSETISTVQEKQKQISPLVRERGPQVAAHITG 128

DB 76 ERSLSLLNCEIKSQEFGVKDML-NKEET-----KKENSFENQKGDQNPQ-IAAHV-- 126

QY 129 TGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIEHKGFFYIY 185

DB 127 -----ISEASKTTSVL-----QW--AEKGYTMSNNLVLTLENGQLGKLVKQGLYIY 172

QY 186 SQTYFRFQEBIKENT-----KNDKQMVQYIYKYVTSYDPDILLMKASRNSCWSKDAEY 237

DB 173 AQVTFCSNRASSQAPFIASLCLKSPQRFER-----ILLRAANTHSAPKPC-- 218

QY 238 GLYSIVQGGIFELKENDRIFSVVTNEHLIDMDHEASFPFG 276

DB 219 GQOSIHLGGVFELQPGASVFVNVTDPQSQVSHGTGFTSFG 257

RESULT 6

A25451

tumor necrosis factor alpha precursor - rabbit

N;Alternate names: cachectin; TNF alpha

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: A25451; J05072

R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayaashi, H.

DNA 5, 149-156, 1986

A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rab

A;Reference number: A25454; MUID:86219711; PMID:3519137

A;Accession: A25454

A;Molecule type: mRNA

A;Residues: 1-234 <ITO>

A;Cross-references: UNIPROT:P04924; GB:M12845; NID:G165759; PIDN:AAA31486.1; PID:G165760

R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.

DNA 5, 157-165, 1986

A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.

A;Reference number: A25451; MUID:86219712; PMID:3519138

A;Accession: A25451

A;Molecule type: DNA

A;Residues: 1-234 <IT2>

A;Note: this sequence differs from that shown in having a Gln inserted between residues

R;Shakhov, A.N.; Kupraev, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.

Gene 95, 215-221, 1990

A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF- α

A;Reference number: JH0309; MUID:91065534; PMID:2249779

A;Accession: JH0309

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-62, 'Q', 63-234 <SHA>

A;Cross-references: GB:M60340; GB:M35326; NID:G165754; PIDN:AAA31484.1; PID:G165756

C;Genetics:

A;Insertions: 62/3; 80/1; 96/1

C;Superfamily: tumor necrosis factor

C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb

F;1-81/Domain: propeptide #status predicted <PRO>

F;92-234/Product: tumor necrosis factor #status predicted <WAT>

F;19,20/Binding site: myristate (lys) (covalent) #status predicted

F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;147-178/Disulfide bonds: #status predicted

Query Match 9.5%; Score 141; DB 1; Length 234;

Best Local Similarity 22.4%; Pred. No. 0.00017;

Matches 62; Conservative 41; Mismatches 98; Indels 76; Gaps 13;

QY 8 GGPQLGTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKQKSGIACFLKEDDSYNDP 67

DB 22 GGPQSKKCLCLSLFSLF-----VAGATTLF-----CLL--HFRVIGP 58

QY 68 NDESNNSPCQVQKQLRQLVRKMI-LRTSEETISTVQEKQKQISPLVRERGPQVAAHI 126

DB 59 QEESEPN-----LHLVNPVAVQMTLRSASRLSD-----KPL-----AHV 94

QY 127 TGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHKGFFYIYS 186

DB 95 VA-----NPOVEGOL-----QWLSQRANALLANGMKLTDNLQVVPADGLYLIYS 138

QY 187 QTYFRFQEBIKENTKNDKQMVQYIYKY-TSYDDPILLMKASRNSCWSKDAEYG-----LY 240

DB 139 QVLFSCQ-----GCRSVLLTHTVSFAVSPYKPKVLLSAIKSPCHRETEAEAPMAWE 193

QY 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEAS-PPG 276

DB 194 PIYLGGVFQLEKGRDLSTEVNQEYLDLAESGVQVYFG 230

RESULT 7

S21738

CD40 ligand - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: S21738

R;Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Macduff, B.

; Cosman, D.; Spriggs, M.K.

Nature 357, 80-82, 1992

A;Title: Molecular and biological characterization of a murine ligand for CD40.

A;Reference number: S21738; MUID:92244364; PMID:1374165

A;Accession: S21738

A;Molecule type: mRNA

F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:146-178/Disulfide bonds: #status predicted

Query Match 8.9%; Score 131; DB 1; Length 234;
Best Local Similarity 20.8%; Pred. No. 0.0012;
Matches 60; Conservative 40; Mismatches 89; Indels 100; Gaps 13;

Qy 8 GPGSLGQTCVLIVFTVLLQSLCAVYVYFTNELKQMDKYSGGIACFL-----K 59
||| : : : : : ||| : : : : :
Db 22 GPGQSRRLCLSLFSPLL---VAGATTLF-----CLLHFGVIGPQR 60
||| : : : : : ||| : : : : :
Qy 60 EDDSYWDPNDEESMNSQWVKQLRQLVRKMLIRTSEETISTVQEKQONISPLVRGP 119
||| : : : : : ||| : : : : :
Db 61 EEQ---PNAFQSN-PLAQT-----LRSSRTPS----- 86
||| : : : : : ||| : : : : :
Qy 120 QRVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRGHSFLNLHRLNGELVTHEK 179
||| : : : : : ||| : : : : :
Db 87 DKPVAHVA-----NPQEGQL--QWLSGRANALLANGVKLTDNQLVPLD 130
||| : : : : : ||| : : : : :
Qy 180 GFYIYYSQYFRQEIEIKTKNDKQMVQYIYKYT-----SYDDPILLMKSARNCSWK 233
||| : : : : : ||| : : : : :
Db 131 GLYLIYSQVLFKQG-----GCPSTHLLTHTISRLAVSYPSKVNLLSAISKSPCHTE 181
||| : : : : : ||| : : : : :
Qy 234 DAIEVG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-PFG 276
||| : : : : : ||| : : : : :
Db 182 SPEQAEAKPYEPIYLGSGVQLEKGDQLSAEINQPNYLDFAESQGVYFG 230
||| : : : : : ||| : : : : :
RESULT 12
S24642
tumor necrosis factor alpha precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: I46047; S24642
R:Cluette, I.; Cluette, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and
A:Reference number: I46046; MUID:94083525; PMID:8260599
A:Cross-references: UNIPROT:Q06599; EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798
A:Accession: I46047
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-233 <CL2>
A:Cross-references: UNIPROT:Q06599; EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798
C:Genetics:
A:Gene: TNFA
A:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: Glycoprotein; lipoprotein; myristylation; transmembrane protein
F:20/Binding site: myristate (lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

Query Match 8.8%; Score 130.5; DB 1; Length 233;
Best Local Similarity 20.3%; Pred. No. 0.0013;
Matches 59; Conservative 43; Mismatches 95; Indels 93; Gaps 13;

Qy 3 MMEVQGPSLGQTCVLIVFTVLLQSLCAVYVYFTNELKQMDKYSGGIACFL----- 58
||| : : : : : ||| : : : : :
Db 17 LSEKAGGPGSRCLSLFSPLL---VAGATTLF-----CLLHFGV 55
||| : : : : : ||| : : : : :
Qy 59 ---KEDDSYWDPNDEESMNSQWVKQLRQLVRKMLIRTSEETISTVQEKQONISPLVR 115
||| : : : : : ||| : : : : :
Db 56 IGQREESPGP---SINSPVQT-----LRSSSQASS----- 85
||| : : : : : ||| : : : : :
Qy 116 ERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRGHSFLNLHRLNGELV 175
||| : : : : : ||| : : : : :
Db 86 ---NKPVAHVA-----DINSPGQLR-----WWDSYANALMANGVKLEDNQLV 125
||| : : : : : ||| : : : : :
Qy 176 IHEKGFYIYYSQYFRQEIEIKTKNDKQMVQYIYK--YTSYDDPILLMKSARNSC--- 230
||| : : : : : ||| : : : : :
Db 126 VPADGLYLIYSQVLFRGQ-----GCPSTPLFHTTISRIVASYQTKNVLISAIKSPCHRE 180
||| : : : : : ||| : : : : :

Search completed: June 22, 2005, 06:03:12
Job time : 28.813 secs

Large Blank (uspio)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 115.832 Seconds
(without alignments)
1242.266 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMEVQGSGSLGQTCVLIV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	1	TN10_HUMAN
2	963	65.2	287	2	Q8K3G0
3	930	62.9	291	1	TN10_MOUSE
4	809.5	54.8	304	2	Q7T1F2
5	577.5	39.1	299	2	Q6DHG9
6	334.5	22.6	317	2	Q7ZVX9
7	307.5	20.8	287	2	Q90WT9
8	305.5	20.7	214	2	Q9DDZ5
9	291	19.7	63	2	Q6JSD9
10	267.5	18.1	318	1	TN11_RAT
11	258.5	17.5	316	1	TN11_MOUSE
12	251.5	17.0	317	1	TN11_HUMAN
13	189.5	12.8	279	1	TNFC_MOUSE
14	187	12.7	280	1	TNFC_CERTO
15	186	12.6	281	1	TN10_HUMAN
16	185	12.5	280	1	TN10_MOUSE
17	185	12.5	280	1	TN10_MOUSE
18	185	12.5	280	1	TN10_MOUSE
19	184.5	12.5	279	2	Q7TWT9
20	184	12.4	272	1	TN10_MOUSE
21	182	12.3	282	1	TN10_MOUSE
22	180	12.2	282	2	Q8K3Y8
23	178.5	12.1	280	2	Q8K1W5
24	177.5	12.0	278	1	TN10_MOUSE
25	175.5	11.9	169	2	Q9W900
26	175	11.8	252	2	Q80Y20
27	173	11.7	252	2	Q8K3Y7
28	166	11.2	251	2	Q8NFE9
29	164	11.1	261	1	TN10_MOUSE
30	163.5	11.1	131	2	Q6J3Q6
31	160	10.8	174	1	TN10_HUMAN

RESULT 1

ID	TN10_HUMAN	STANDARD;	PRT;	281 AA.
AC	P50591;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).			
GN	Names=TNFSP10; Synonyms=APO2L, TRAIL;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;			
RA	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A., Goodwin R.G.;			
RA	Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A., Goodwin R.G.;			
RT	"Identification and characterization of a new member of the TNF family that induces apoptosis."			
RL	Immunity 3:673-682(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=96278649; PubMed=8663110; DOI=10.1074/jbc.271.22.12687;			
RA	Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A., Ashkenazi A.;			
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family."			
RL	J. Biol. Chem. 271:12687-12690(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymph;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner K.H., Sherman C.M., Schuler G.D., Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madao A., Rodriguez S., Sanchez A., Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.

RX MEDLINE=20017054; PubMed=1054288; DOI=10.1016/S1097-2765(00)80207-5;

RA Hymowitz S.G., Christinger H.W., Fuh G., Ulsch G., O'Connell M.,

RA Kelley R.F., Ashkenazi A., de Vos A.M.;

RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a

RT complex with death receptor 5.";

RL Mol. Cell 4:563-571(1999).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.

RX PubMed=10542098; DOI=10.1038/14935;

RA Mongkoleapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,

RA Jones E.Y., Screaton G.R.;

RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring

RT specificity in apoptotic initiation.";

RL Nat. Struct. Biol. 6:1048-1053(1999).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.

RX MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;

RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,

RA Sung Y.C., Oh B.-H.;

RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with

RT selective antitumor activity.";

RL Immunity 11:253-261(1999).

CC -I- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,

CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and

CC possibly also to TNFRSF10E/OPG. Induces apoptosis. Its activity

CC may be modulated by binding to the decoy receptors

CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF10E/OPG that cannot

CC induce apoptosis.

CC -I- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per

CC trimer.

CC -I- SUBUNIT: Homotrimer.

CC -I- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

CC -I- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung

CC and prostate.

CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC -----

DR EMBL; U37518; AAC50332.1; -.

DR EMBL; U57059; AAB01233.1; -.

DR EMBL; BC032722; AH32722.1; -.

DR PDB; 1D0G; X-ray; A/B/D=114-281.

DR PDB; 1D2Q; X-ray; A=114-281.

DR PDB; 1D4V; X-ray; B=119-281.

DR PDB; 1DG6; X-ray; A=91-281.

DR PDB; 1DU3; X-ray; D/E/F/J/K/L=114-281.

DR Genew; HGNC:11925; TNFSF10.

DR H-InvDB; HIX0003863; -.

DR MIM; 603598; -.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0005625; C:soluble fraction; TAS.

DR GO; GO:0005102; P:receptor binding; TAS.

DR GO; GO:0007267; P:cell-cell signaling; TAS.

DR GO; GO:0006917; P:induction of apoptosis; TAS.

DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB; IEP.

DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR006052; TNF family.

DR InterPro; IPR008983; TNF-like.

DR InterPro; IPR001636; TNF_subf.

DR Pfam; PF00229; TNF; 1.

DR ProDom; PD002012; TNF_subf; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS0049; TNF_2; 1.

KW 3D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor; Transmembrane; Zinc.

FT DOMAIN 1 17 Cytoplasmic (Potential).

FT TRANSMEM 18 38 Signal-anchor for type II membrane protein (Potential). Extracellular (Potential). Zinc.

FT DOMAIN 39 281

FT METAL 230 230

FT STRAND 123 127

FT STRAND 149 150

FT STRAND 163 165

FT STRAND 167 170

FT TURN 171 172

FT STRAND 173 176

FT STRAND 180 193

FT TURN 198 199

FT STRAND 205 213

FT STRAND 220 228

FT TURN 233 234

FT STRAND 237 250

FT TURN 252 253

FT STRAND 255 260

FT HELIX 263 265

FT STRAND 266 267

FT TURN 270 272

FT STRAND 274 279

SQ SEQUENCE 281 AA; 32509 MW; DAAAF78DAAB2F6D CRC64;

Query Match 100.0%; Score 1478; DB 1; Length 281;

Best Local Similarity 100.0%; Pred. No. 4.4e-113;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60

DB 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60

QY 61 DSYNDPNDDESNPCWQKWLQRLVRKMLRTSEETISTVQEKQKNISPLVRGPG 120

DB 61 DSYNDPNDDESNPCWQKWLQRLVRKMLRTSEETISTVQEKQKNISPLVRGPG 120

QY 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180

DB 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180

QY 181 FVYISQTYFRQEEIKENTKNDKQWQVYKYTSYPDPILLMKSNCSKDAEYGLY 240

DB 181 FVYISQTYFRQEEIKENTKNDKQWQVYKYTSYPDPILLMKSNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 2

ID Q8K3G0 PRELIMINARY; PRT; 287 AA.

AC Q8K3G0;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

OS TNF-related apoptosis inducing ligand.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DA;

RA Mueller A.M., Giegerich G.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY115578; AAM49797.1; -.

DR HSSP; PS0591; 1DQ.

DR GO; GO:0016020; C:membrane; IEA.


```
DR HSP; P50591; 1D2Q.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 54.8%; Score 809.5; DB 2; Length 304;
Best Local Similarity 55.4%; Pred. No. 3.6e-58;
Matches 160; Conservative 45; Mismatches 65; Indels 19; Gaps 6;

QY 8 GGPSLGGTCLVIFVTLVQLSCVAVTVYFTNELKQMDKYSKSGIACFLKEDDSYMDP 67
Db ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5 GGFSPARTCGAVLVAALLQSCVAVTVYFTNELKQLMDTYSRGTACLTGELGLDIQ 64
QY 68 N-----DESMNPGQVQKQLRQVRKMLRTSEETISVQ-EKQNIPLVRGPO- 120
Db ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
65 NLDVVESKORVADPCQVQVHGLKLIKQMSRILOENMSAINGDRQTQALSR--RDEPPQG 122
QY 121 ---RVAHLITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVTH 177
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
123 PTLRIAAHLTGSSKSSA-SPHYLSYRGIGHKHSWESSRSGHSFLYNVELMNGELVLP 181
QY 178 EKGFFIYSQTYRFOFE-----IKENTKNDQMVQYIYKYTSPDPILLMKASNSCW 231
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
182 QTGFYIYSQTYRFRNEDEDSGLLERIKNPQLVQYIKLTNYDPDILLMKASNTSCW 241
QY 232 SKDAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 280
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
242 SKKAEGLYSIYQGGVQLKREDRIEFVSVNSDIVDMDEKASFFGAFIM 290

RESULT 5
Q6DHG9 PRELIMINARY; PRT; 299 AA.
AC Q6DHG9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Zgc:92320.
GN Name=zgc:92320;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.C., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
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RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076005; AAH76005.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF_like.
DR InterPro; IPR008983; TNF_family.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 299 AA; 33526 MW; BA776793D2F11ED5 CRC64;

Query Match 39.1%; Score 577.5; DB 2; Length 299;
Best Local Similarity 42.2%; Pred. No. 3.9e-39;
Matches 121; Conservative 57; Mismatches 82; Indels 27; Gaps 8;

QY 18 LIVIFVTLVQLSCVAVTVYFTNELKQMDKYSKSGIACFLKED---DSVWDPNDESXN 74
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
15 LLLLAAILQTTAVAVTFYFNSVLTMTKETSKSVSCIMRANLRTIKGQELNGAEGKD 74
QY 75 SPCWQVQKQLRQVRK-MILRTSEETISVQSKQKNISPLV-----RERGPORVAAHITG 128
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
75 DFCWQVQQLHFLIEKSMSSRYQKEITSVAVKDEVSRLVSLVQLQDQEDSSRPKIAHVTG 134
QY 129 TGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHIEKGFYIYSQT 198
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
135 SYTPSEKDGAGLPNRKVYQGIQSWESK-GLAFLQNVLSLQDGLVLPQAGLYIYSQT 193
QY 189 YFR---FQEEIKENTKND-----KQWQVIY-KYTSYDPDILLMKASNSCW 233
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
194 YFRHTLIEED--ESAREDEYSGMSGVSVRGKPLQVYVKKVSYQVDPILLMKARTCN 251
QY 234 DAEGYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 280
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
252 DSEYGLYSIYQAGLQGLGSGDRVFTVSVNSVSTIDMDKSSFFGAFIV 298

RESULT 6
Q7ZYX9 PRELIMINARY; PRT; 317 AA.
AC Q7ZYX9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tnfsf101 protein.
GN Name=tnfsf101;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strauberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044336; AA444336.1; -.
DR HSSP; P50591; ID20
DR ZFIN; ZDB-GENE-010801-1; tnfsf101.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DC9F CRC64;
Query Match 22.6%; Score 334.5; DB 2; Length 317;
Best Local Similarity 29.2%; Pred. No. 3.7e-19;
Matches 83; Conservative 55; Mismatches 113; Indels 33; Gaps 8;
QY 18 LIVFTVLLQSLCAVAVTVYVFTHELKQMDKQKYSKGACF-----LKEDSYNDPND-EE 71
DB 40 MVIVVVVVLQIASTTGLFVYLNMSLSQVSGVTEELRLGLNLVGLKQDDI--PEDLAQ 97
QY 72 SMNSPCQVQWQLRQLVRKM-----ILRTSEETISTVQEKQNIPLVRERGQ 120
DB 98 LFGEPCMKLAGIKAYISKVTDSTLSIKQTHAARTRTHSYNTGSKMTTV-----MQ 150
QY 121 RVAAHITGTRGRSNT-----LSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 175
DB 151 RPSAHLTSSASDNSRPSQDMHQPDQLHQSCRHPVHTW-ANKSFGAHLNMTLTNGRLR 209
QY 176 IHEKGFYIYSQYFRP-QBEIKENTKNDKQVQIYKYTSYDPDILLMKSAKNSCKD 234
DB 210 VPQDGRYLYSQVYFRYFSPSPSDQSSVSHQLVQCIYKTSYLNPIQLLKGVGKTCWAPD 269
QY 235 AEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASPFQAF 278
DB 270 AEYALHSYQGLFELKAGDEVFVSVSSPTWVGEDSSSYFGAF 313
RESULT 7
Q90WT9
ID Q90WT9 PRELIMINARY; PRT; 287 AA.
AC Q90WT9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TNF-related apoptosis inducing ligand-like protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

RA Bridgham J.T., Johnson A.L.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057941; AAU23702.1; -.
DR HSSP; P50591; ID20.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 287 AA; 37092 MW; DB06E1C95087B108 CRC64;
Query Match 20.8%; Score 307.5; DB 2; Length 287;
Best Local Similarity 32.3%; Pred. No. 5.3e-17;
Matches 93; Conservative 46; Mismatches 110; Indels 39; Gaps 11;
QY 18 LIVFTVLLQ-SLCVAVTVYVFT-----NELKQW--ODKYSKSGIACFLKEDDSYWD 66
DB 8 LLHAFSLEQLLPLCTAPEWAGTWSQALQGNAPPRKAGSQSSSEELRCLQLINQQEG 67
QY 67 PNDEESM-NSPCQVQWQLRQLVRKMLRTSEETI--STVQEKQ---NISP-LVREGRP 119
DB 68 SNLEELISNQSC---LKLANTIKAVVATVTENVISRVNEAQSIFYNISEGQVATKTL 123
QY 120 QRVAHI-----TGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLR 170
DB 124 GKPSAHLIFRPQNPQPAQDGSRRFGNLS-----QSCRHAITRWEDS-TIHSILQNTYR 175
QY 171 NGELVTHEKGFYIYSQYFRFOEIKENTKNDKQVQIYKYTSYDPDILLMKSAKNSC 230
DB 176 DGLRNVNQAGKYIYQIYFRYSRQDAGARVSVPLVQCVQCNWKTYSQPIQLLKGVGKTC 235
QY 231 WSKDARYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASPFQAF 278
DB 236 WAEAEYGLHALYQGLFELKAGDELFSVSVSLAIDYSDAAASYFGAF 283
RESULT 8
Q9DDZ5
ID Q9DDZ5 PRELIMINARY; PRT; 214 AA.
AC Q9DDZ5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TRAIL-like protein.
GN Name:tnfsf101;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "Molecular cloning and expression of a TNF receptor and two TNF
RT ligands in the fish ovary."
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
DR EMBL; AF250041; AAG47640.1; -.
DR HSSP; P50591; ID20.
DR ZFIN; ZDB-GENE-010801-1; tnfsf101.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Query Match	20.7%;	Score 305.5;	DB 2;	Length 214;
Best Local Similarity	37.6%;	Pred. No. 5.3e-17;		
Matches	62;	Conservative 37;	Mismatches 59;	Indels 7; Gaps 3;
QY	120	ORVAAHITGRSNT-----LSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGEL	174	
DB	47	QPSAHLTSSADNSRQSDKHQFQDLHSGCRHPVHTW-ANKSFGAHLNMTLTNGRL	105	
QY	175	VHKEGFFYIYSQTYFRF-QEEIKENTKNDKQWQYIYKTSYDPDPILLMKASRNSQWSK	233	
DB	106	RVPQGRYLYSQVFRYPSRSDSQSSVSHQVLCVCIYKTSYLNPTQLLKGVTGKCAP	165	
QY	234	DARYGLYSIQGIFELKENDRIFVSTNEHLIDMDHEASFPFGAF	278	
DB	166	DABYALHSVYQGLFELRAGDEVFVSPTWYGEDSSSYFGAF	210	
RESULT 9				
Q6JSD9		PRELIMINARY;	PRT;	63 AA.
ID	Q6JSD9			
AC	Q6JSD9			
DT	05-JUL-2004	(T-EMBLrel. 27, Created)		
DT	05-JUL-2004	(T-EMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(T-EMBLrel. 27, Last annotation update)		
DE	Chemokine tumor necrosis factor ligand superfamily member 10			
DE	(Fragment)			
GN	Name=TNFSF10;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung carcinoma;			
RA	Polvi A., Ruoslahti S., Vendelin J., West A., Saarikko I.,			
RA	Reinkainen A., Hollmen J., Laitinen T., Mannila H., Laheesmaa R.,			
RA	Kere J.,			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AV312579; AAR16184.1; -			
FT	NON_TER 1 1			
SQ	SEQUENCE 63 AA; 7638 MW; 8F0C7933DA5AA6B6 CRC64;			
Query Match	19.7%;	Score 291;	DB 2;	Length 63;
Best Local Similarity	100.0%;	Pred. No. 1.7e-16;		
Matches	52;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	39	TNELKQMDKYSKSGIACFLKEDDSYWDNDSESNMSPCWQYKQLRLVRK 90		
DB	1	TNELKQMDKYSKSGIACFLKEDDSYWDNDSESNMSPCWQYKQLRLVRK 52		
RESULT 10				
TN11 RAT		STANDARD;	PRT;	318 AA.
ID	TN11 RAT			
AC	Q9SE2; Q91219;			
DT	28-FEB-2003	(Rel. 41, Created)		
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	03-JUL-2004	(Rel. 44, Last annotation update)		
DE	Tumor necrosis factor ligand superfamily member 11 (Receptor activator			
DE	of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-			
DE	induced cytokine factor) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast			
DE	differentiation factor) (ODF)			
GN	Name=TNfsf11; Synonyms=Oppl, Rankl, Trance;			
OS	Rattus norvegicus (Rat)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Tibial bone;			
RA	Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,			

QY 62 -DSYWPNDSESNVSCWQVWQLRQLVRXMIILTSEETISTVQFKQONISPLVRERGPO 120
 DB 101 QDSTLESETEALPDCRRMKQAFQ-----GAVORELOHIV-----GPO 139
 QY 121 R---VAAHITG-----RGRS-----NTLSSPNSKNEKALGRKINSWESSRSGH 161
 DB 140 RFGCVPMWEGSWLDVARRGKPAQPAFHLITNAADIPSGSHKVSU-----SSWYHR-GW 194
 QY 162 SFLSNLHLRNGELVILHEKGFFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYT-SYPDPI 220
 DB 195 AKISNMTLSGKLVRQDGFYLYANICFRHHTSGSVPADYQLQVMVYVVKTSIKIPSSH 254
 QY 221 LLMKSARNCSWDAEYGLYSIQGIFELKENDRIFSVSTNEHLIDMDHEASPRCAFV 280
 DB 255 NLMKGGSTKNWGSNGBFHYFVINGVGFKL RAGEEISVQVNSPLDPODATYFGAFKV 314

RESULT 11

TN11_MOUSE STANDARD; PRT; 316 AA.

AC O35235; O35306; Q9JJK8; Q9JJK9; Q9RIY0;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
 DE (OCIF).
 GN Name=Tnfrsf11; Synonyms=OPGL, RANKL, Trance;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hybridoma;
 RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells.";
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thymic lymphoma;
 RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
 RA Anderson D.N., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometsko M.S., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
 RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow;
 RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
 RA Boyle W.J.;
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
 RT differentiation and activation.";
 RL Cell 93:165-176(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow stroma;
 RX MEDLINE=98198248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M.,
 RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto K., Murakami A., Tsuda E.,

RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
 RT "Osteoclast differentiation factor is a ligand for
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
 RL to TRANCE/RANKL.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=129;
 RX MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
 RA Ueda M., Higashio K.;
 RT "Cloning and characterization of the gene encoding mouse osteoclast
 RT differentiation factor.";
 RL Gene 230:121-127(1999).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
 RT "Determination of three isoforms of the receptor activator of nuclear
 RT factor-kappaB ligand and their differential expression in bone and
 RT thymus.";
 RL Endocrinology 142:1419-1426(2001).
 RN [7]
 RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
 RX MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
 RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
 RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
 RT "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
 RT converting enzyme-like protease in shedding of TRANCE, a TNF family
 RT member involved in osteoclastogenesis and dendritic cell survival.";
 RL J. Biol. Chem. 274:13613-13618(1999).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
 RX MEDLINE=21464816; PubMed=11581298;
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
 RT of receptor-ligand specificity.";
 RL J. Clin. Invest. 108:971-979(2001).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
 RX MEDLINE=21939021; PubMed=11733492; DOI=10.1074/jbc.M106525200;
 RA Ito S., Wakabayashi K., Ubukata O., Hayaishi S., Okada T.;
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at
 RT 2.2-A resolution.";
 RL J. Biol. Chem. 277:6631-6636(2002).
 CC -I- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcaemia of malignancy.
 CC -I- SUBUNIT: Homotrimer.
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein and secreted
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O35235-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O35235-2; Sequence=VSP_006449;
 CC Name=3;
 CC IsoId=O35235-3; Sequence=VSP_006448;
 CC -I- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
 CC but not in nonlymphoid tissues and is abundantly expressed in T
 CC cells but not in B cells. A high level expression is also seen in
 CC the trabecular bone and lung.
 CC -I- PTM: N-glycosylated.
 CC -I- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing. The cleavage may be catalyzed by
 CC ADAM17. A further shorter soluble form was observed.
 CC -I- DISEASE: Deficiency in Tnfrsf11 results in failure to form lobulo-

RESULT 14
TNF6_CERTO STANDARD; PRT; 280 AA.
AC Q9BDN1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN Names=TNFSF6; Synonyms=CD95L, FASL;
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/FasL ligand and co-stimulatory molecules";
RL Immunogenetics 53:315-328(2001).
CC -!- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/CD93
CC modulates its effects (By similarity).
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF344847; AAK37606.1; ..
CC HSP: P50591; I2DQ
CC InterPro: IPR08064; Fas_ligand.
CC InterPro: IPR06053; TNF_abc.
CC InterPro: IPR06052; TNF family.
CC InterPro: IPR008983; TNF like.
CC InterPro: IPR003636; TNF_subf.
CC Pfam: PF00229; TNF; 1
CC PRINTS: PR01681; FASLIGAND.
CC PRINTS: PR01234; TNFCROSFCT.
CC ProDom: PD02012; TNF_subf; 1.
CC SMART: SM00207; TNF; 1.
CC PROSITE: PS00251; TNF; 1.
CC PROSITE: PS50049; TNF; 2; 1.
KW Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
FT CHAIN 1 280 Tumor necrosis factor ligand superfamily
FT member 6, membrane form.
FT CHAIN 129 280 Tumor necrosis factor ligand superfamily
FT member 6, soluble form (By similarity).
FT DOMAIN 1 80 Cytoplasmic (Potential).
FT TRANSMEM 81 101 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 102 280 Extracellular (Potential).
FT DOMAIN 4 69 Pro-rich.
FT DOMAIN 45 64 Poly-Pro.
FT SITE 128 129 Cleavage (By similarity).
FT DISULFID 201 232 Potential.

FT CARBOHYD 183 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 249 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 259 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;
Query Match 12.7%; Score 187; DB 1; Length 280;
Best Local Similarity 22.1%; Pred. No. 4e-07;
Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;
QY 4 MEVQGPSLGQTCVLIVITVLLQSLCAVYVYFTNELKMQDKYSKGIACFLKEDDS 63
Db LKRGHNHSTG-LCLLVMPFWLVALVGLGLGMPQLFHLQKELAE-----LRST 118
QY 64 YNDPNDSESNPCWQVKQLRQVRLRSEETISTVQEKQNIPLVRGPGORVA 123
Db QKHTASLEKQIGHPSP-PPEKQKQKV 145
QY 124 AHITGRGRSNTLSSPNSKNEKALGRKINSWSSRGHGFSLNHLRNGELVTHEKGFY 183
Db AHLTG-----KNSRSMPL-----EWEDT-YGIVLLSGVKYKGGVLINETGLYF 189
QY 184 IYSQTYFRFQEEIKENTKNDKQVQYIY-KYTSYDPPIILMKMSARNSCKDAEYGLYSI 242
Db VYSKVYFRQ-----SCTNLPLSHKVMYRNNSKYQDVLVMEGKQMS-YCTTGQMAHSS 242
QY 243 YQGGIFELKENRIFVSVTNEHLIDMDHEASFGAP 278
Db YLGAVENTLTDLHYVNVSELSLVNPFESQTFPGLY 278
RESULT 15
TNF6_HUMAN STANDARD; PRT; 281 AA.
AC P48023; Q9BZP9;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (Apoptosis antigen ligand) (APTL) (CD178 antigen).
GN Names=TNFSF6; Synonyms=APTLG1, FASL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
RT lymphocytes";
RL J. Exp. Med. 181:71-77(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: Gene structure, chromosomal location and species
RT specificity";
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Schaezel C.E., Pohlmann R., Philippson P., Eibel H.;
RN Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayaehi N., Iio S., Takehara T., Hijioaka T., Kasahara A.,
RA Fusamoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT infection";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;

RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;
 RT "Isolation and characterization of a new naturally occurring variant of
 RT human Fas ligand that is expressed only in membrane bound form.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Wilkinson J.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klugner R.D., Collins F.S., Buetow K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Blood;
 RA Matsumura M., Nakanishi Y., Ohba Y.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TVR-218 AND PHE-275.
 RX MEDLINE=97373583; PubMed=9228058; DOI=10.1074/jbc.272.30.18827;
 RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
 RA Terskikh A., Peitsch M.C., Tschopp J.;
 RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
 RL J. Biol. Chem. 272:18827-18833(1997).
 RN [10]
 RP PROCESSING.
 RX MEDLINE=98087475; PubMed=9427603;
 RA Tanaka M., Itai T., Adachi M., Nagata S.;
 RL "Downregulation of Fas ligand by shedding.";
 Nat. Med. 4:31-36(1998).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
 CC modulates its effects.
 CC -!- SUBUNIT: Homotrimer (Probable).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released
 CC into the extracellular fluid, probably by cleavage from the cell
 CC surface.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P48023-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P48023-2; Sequence=VSP_006443, VSP_006444;
 CC -!- PTM: N-glycosylated.
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing.
 CC -!- DISEASE: Defects in TNFRSF6 are a cause of autoimmune
 CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
 CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome

CC involving hemolytic anemia and thrombocytopenia with massive
 CC lymphadenopathy and splenomegaly.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -!- DATABASE: NAME=PROW; NOTE=PROW 2;59-69(2001);
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X89102; CAA61474.1; -;
 CC EMBL; U08137; AAC50071.1; -;
 CC EMBL; U11821; AAC50124.1; -;
 CC EMBL; D38122; BAA07320.1; -;
 CC EMBL; AF288573; AAG60017.1; -;
 CC EMBL; Z96050; CAB09424.1; -;
 CC EMBL; BC017502; AAH17502.1; -;
 CC EMBL; AB013303; BAA32542.1; -;
 CC EIR; I38707; I38707.
 CC HSSP; P50591; ID20.
 CC Genew; HGNC:11936; TNFRSF6.
 CC H-InVDB; HIX0001337; -;
 CC MIM; 134638; -;
 CC MIM; 601859; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0005102; F:receptor binding; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0006917; P:induction of apoptosis; TAS.
 CC GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB; IEP.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR008064; Fas_ligand.
 CC InterPro; IPR006053; TNF_abc.
 CC InterPro; IPR006052; TNF family.
 CC InterPro; IPR008983; TNF like.
 CC InterPro; IPR003636; TNF_subf.
 CC Pfam; PF00229; TNF; 1.
 CC PRINTS; PRO1681; FASLIGAND.
 CC PRINTS; PRO1234; TNECROSISPT.
 CC ProDom; PD002012; TNF_subf; 1.
 CC PROSITE; PS00251; TNF 1; 1.
 CC PROSITE; PS50049; TNF 2; 1.
 CC Alternative splicing; Antigen; Apoptosis; Cytokine; Glycoprotein;
 CC Signal-anchor; Transmembrane.
 CC CHAIN 1 281
 CC Tumor necrosis factor ligand superfamily
 CC member 6, membrane form.
 CC Tumor necrosis factor ligand superfamily
 CC member 6, soluble form.
 CC Cytoplasmic (Potential).
 CC Signal-anchor for type II membrane
 CC protein (Potential).
 CC Extracellular (Potential).
 CC Pro-rich.
 CC Poly-Pro.
 CC Cleavage.
 CC Potential.
 CC N-linked (GlcNAc...) (Potential).
 CC N-linked (GlcNAc...) (Potential).
 CC N-linked (GlcNAc...) (Potential).
 CC STSQMHTASSL -> ATPVHLKRS (in isoform
 CC 2).
 CC /FTID=VSP_006443.
 CC Missing (in isoform 2).
 CC /FTID=VSP_006444.
 CC P->D,F,R: Lowers binding to TNFRSF6 and
 CC reduces cytotoxicity more than 100-fold.
 CC Y->F,R: Lowers binding to TNFRSF6 and
 CC abolishes cytotoxicity.
 CC F->L: Abolishes binding to TNFRSF6 and
 CC cytotoxicity.
 CC
 CC CHAIN 130 281
 CC DOMAIN 1 80
 CC TRANSMEM 81 102
 CC DOMAIN 103 281
 CC DOMAIN 4 70
 CC DOMAIN 45 65
 CC SITE 129 130
 CC DISULFID 202 233
 CC CARBOHYD 184 184
 CC CARBOHYD 250 250
 CC CARBOHYD 260 260
 CC VARSPLIC 117 127
 CC
 CC VARSPLIC 128 281
 CC MUTAGEN 206 206
 CC MUTAGEN 218 218
 CC MUTAGEN 275 275

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 124.948 Seconds
(without alignments)
869.796 Million cell updates/sec

Title: US-10-662-429-2
Perfect score: 1478
Sequence: 1 MANMEVQGSPSLGQTCLVIV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1980s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	2	AAW19777 Novel cyt
2	1478	100.0	281	2	AAW27134 Human Apo
3	1478	100.0	281	2	AAW19787 Human apo
4	1478	100.0	281	2	AAW76829 Human TL2
5	1478	100.0	281	2	AAW56760 Human TRA
6	1478	100.0	281	2	AAW44354 Human AGP
7	1478	100.0	281	2	AAW01517 Protein a
8	1478	100.0	281	2	AAW27012 Human Apo
9	1478	100.0	281	3	AAW81956 Human Apo
10	1478	100.0	281	3	AAW24038 Human PRO
11	1478	100.0	281	3	AAW08545 Amino aci
12	1478	100.0	281	3	AAW28691 Human AGP
13	1478	100.0	281	4	AAW50977 Human PRO
14	1478	100.0	281	4	AAW67243 Human Apo
15	1478	100.0	281	4	AAW11031 Human TNF
16	1478	100.0	281	4	AAW48350 Human TL2
17	1478	100.0	281	5	AAW08133 Human TRA
18	1478	100.0	281	5	AAW31630 Human TRA
19	1478	100.0	281	5	AAW75062 Human TNF
20	1478	100.0	281	5	AAW51077 Human Apo
21	1478	100.0	281	5	AAW51954 Human Apo
22	1478	100.0	281	5	AAW019095 C neoform
23	1478	100.0	281	5	AAW79593 Human TNF
24	1478	100.0	281	5	AAW73861 Human Apo
25	1478	100.0	281	6	ABU10205 Human Apo

26	1478	100.0	281	6	ABU71443 Human neo
27	1478	100.0	281	6	ABG72738 Human TNF
28	1478	100.0	281	6	AAO29543 Human TRA
29	1478	100.0	281	6	ABU08558 Human TNF
30	1478	100.0	281	6	ABR42313 Human TRA
31	1478	100.0	281	6	ABG71905 Human TRA
32	1478	100.0	281	6	ABP60546 Human tum
33	1478	100.0	281	6	AAE36258 Human TRA
34	1478	100.0	281	6	AAO31151 Human TNF
35	1478	100.0	281	6	ABO25125 Human TNF
36	1478	100.0	281	7	ADB61471 Native hu
37	1478	100.0	281	7	ADC35202 Human TNF
38	1478	100.0	281	7	ADD14080 Human arc
39	1478	100.0	281	7	ADD19010 Human dis
40	1478	100.0	281	7	ABW02276 Human TRA
41	1478	100.0	281	8	ADE76953 Human pro
42	1478	100.0	281	8	ADK72311 Human Apo
43	1478	100.0	281	8	ADK72303 Human Apo
44	1478	100.0	281	8	ADK72304 Human Apo
45	1478	100.0	281	8	ADK72296 Human wil

ALIGNMENTS

RESULT 1
AAW19777

ID :AAW19777 standard; protein; 281 AA.

XX	AC	AAW19777;			
DT	22-SBP-1997	(first entry)			
XX	DE	Novel cytokine Apo-2 ligand.			
XX	KW	Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.			
XX	OS	Homo sapiens.			
XX	FH	Key	Location/Qualifiers		
FT	Peptide	1..281	/note= "Claim 4"		
FT	Region	1..14	/label= Cytoplasmic_region		
FT	Protein	15..281	/note= "Claim 3"		
FT	Region	15..40	/label= Transmembrane_region		
FT	Protein	41..281	/note= "Claim 2"		
FT	Region	41..281	/label= Extracellular_region		
FT	Modified-site	109	/label= Glycosylation		
FT	Protein	114..281	/note= "putative N-linked glycosylation site"		
FT			/note= "Claim 1"		

WO9725428-A1.

17-JUL-1997.

08-JAN-1997; 97WO-US000272.

09-JAN-1996; 96US-00584031.

(GETH) GENENTECH INC.

Ashkenazi AJ, Chuntharapai A, Kim KJ;

WPI; 1997-372867/34.

N-PSDB; AAT72796.

PT Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
 PT apoptosis for the treatment of breast and colon cancer.
 XX
 PS Claim 4; Fig 1a; 72pp; English.
 XX
 CC A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian
 CC cell apoptosis. It is believed to be a member of the tumour necrosis
 CC factor cytokine family. Its amino acid sequence was deduced from a cDNA
 CC clone (AAT72796) isolated from a human placental cDNA library. Apo-2
 CC ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
 CC 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
 CC transformed or transfected with a vector contg. Apo-2 ligand nucleic
 CC acid. They can be used to induce apoptosis in mammals and to treat
 CC pathological conditions such as cancer (esp. breast or colon cancer) or
 CC to raise antibodies useful in diagnostic assays
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMVEVQGGPSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMVEVQGGPSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESNPCWQVKQLRVKMLRTSEETISTVQEKQNIPLVRERGQ 120
 DB 61 DDSYWDPNDESNPCWQVKQLRVKMLRTSEETISTVQEKQNIPLVRERGQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 RESULT 2
 AAW27134
 ID AAW27134 standard; protein; 281 AA.
 XX
 AC AAW27134;
 XX
 DT 02-APR-1998 (first entry)
 XX
 DE Human Apoptosis inducing molecule-I (AIM-I).
 XX
 KW Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
 KW tumour necrosis factor ligand superfamily; AIM-I altered expression;
 KW neoplasia inhibition; anti-inflammatory agent.
 XX
 OS Homo sapiens.
 XX
 PN WO9733899-A1.
 XX
 PD 18-SEP-1997.
 XX
 PF 14-MAR-1996; 96WO-US003773.
 XX
 PR 14-MAR-1996; 96WO-US003773.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM;
 XX
 DR WPI; 1997-470807/43.
 DR N-PSDB; AAT85210.

XX
 PT New isolated apoptosis inducing molecule-I - used to develop products for
 PT the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
 PT versus host disease or inflammation.
 XX
 PS Claim 2; Fig 1; 82pp; English.
 XX
 CC The present sequence represents a human Apoptosis inducing molecule-I
 CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand
 CC superfamily. The products can be used in the diagnosis and treatment of
 CC disorders related to under-expression, over-expression or altered
 CC expression of AIM-I. AIM-I or agonists can be used for treating
 CC autoimmune disorders including systemic lupus erythematosus,
 CC immunoproliferative disease lymphadenopathy (IPL),
 CC angioimmunoproliferative disease lymphadenopathy (AIL), rheumatoid arthritis,
 CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit
 CC neoplasia such as tumour cell growth, to treat restenosis, to regulate
 CC haematopoiesis in endothelial cell development, to stimulate peripheral
 CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
 CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or
 CC osteoporosis, for preventing graft-host rejection, and as anti-
 CC inflammatory agents, for treating endotoxic shock or to prevent
 CC activation of HIV
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMVEVQGGPSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMVEVQGGPSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESNPCWQVKQLRVKMLRTSEETISTVQEKQNIPLVRERGQ 120
 DB 61 DDSYWDPNDESNPCWQVKQLRVKMLRTSEETISTVQEKQNIPLVRERGQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 RESULT 3
 AAW19787
 ID AAW19787 standard; protein; 281 AA.
 XX
 AC AAW19787;
 XX
 DT 24-SEP-1997 (first entry)
 XX
 DE Human apoptosis inducer cytokine TRAIL.
 XX
 KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
 KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
 KW thrombotic microangioplasty; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Domain 1..18
 FT Domain /label= Cytoplasmic_domain
 FT Domain 19..38
 FT Domain /label= Transmembrane_domain
 FT Domain 39..281

FT /label= Extracellular domain
 FT /note= "contains a receptor-binding region"
 FT 89..90
 FT Cleavage-site
 FT /note= "potential KEX2 protease processing site"
 FT 109..111
 FT Modified-site
 FT /note= "potential N-glycosylation site"
 FT 149..150
 FT Cleavage-site
 FT /note= "potential KEX2 protease processing site"
 FT W09701633-A1.
 PN 16-JAN-1997.
 XX 25-JUN-1996; 96WO-US010895.
 XX 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548368.
 XX (IMMUNEX CORP.
 XX WILEY SR, Goodwin RG;
 XX WPI; 1997-118715/11.
 DR N-PSDB; AAT72847.
 XX TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
 PT cells - useful for treating thrombotic microangiopathy, cancer and viral
 FT infection and for use in assays.
 XX Claim 10; Page 43-44; 62pp; English.
 XX Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
 CC (AAW19787) is a novel cytokine that induces apoptosis of certain target
 CC cells, including cancer cells and virally infected cells. Its amino acid
 CC sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in
 CC vector pBC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
 CC polypeptides) can be expressed in host cells and used in the treatment of
 CC cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
 CC to raise antibodies that may be useful for treating thrombotic
 CC microangiopathies
 XX Sequence 281 AA;
 SQ
 Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGTCLVIFVTLVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGTCLVIFVTLVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDNDDESNMPCWQVKQLRQLVRKWLRTSEETISTVQEKQONISPLVRRGPQ 120
 DB 61 DDSYWDNDDESNMPCWQVKQLRQLVRKWLRTSEETISTVQEKQONISPLVRRGPQ 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDPDPILLMKSARNCSWDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDPDPILLMKSARNCSWDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 RESULT 4
 AAW76829
 ID AAW76829 standard; protein; 281 AA.
 XX
 AC AAW76829;

XX 25-JAN-1999 (first entry)
 DT Human TL2 protein.
 XX TR6; tumour necrosis factor related receptor; human; treatment; stroke;
 KW inflammation; arthritis; septicaemia; autoimmune disease; restenosis;
 KW transplant rejection; infection; ischaemia; brain injury; bone disease;
 KW acute respiratory disease syndrome; acquired autoimmune disease syndrome;
 KW AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF;
 KW TL2. tumour necrosis factor-related apoptosis-inducing ligand.
 OS Homo sapiens.
 XX EP870827-A2.
 XX 14-OCT-1998.
 XX 23-DEC-1997; 97EP-00310562.
 XX 14-MAR-1997; 97US-0041230P.
 PR 09-MAY-1997; 97US-00853684.
 PR 22-AUG-1997; 97US-00916625.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Deen KC, Young PR;
 PI WPI; 1998-523156/45.
 DR N-PSDB; AAV63096.
 XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding
 PT polypeptide, antibody, agonist, antagonist, etc.
 XX Disclosure; Page 32-33; 34pp; English.
 CC This sequence represents the human tumour necrosis factor (TNF)-related
 CC receptor, TR6 (also known as tumour necrosis factor-related apoptosis-
 CC inducing ligand, TRAIL). This protein is used in a method resulting in
 CC the isolation of the novel human TNF related receptor, TR6. TR6
 CC polypeptides and polynucleotides can be used in the treatment of chronic
 CC and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g.
 CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
 CC host disease, infection, stroke, ischaemia, acute respiratory disease
 CC syndrome, restenosis, brain injury, (acquired autoimmune disease
 CC syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative
 CC disorders), atherosclerosis and Alzheimers disease
 XX Sequence 281 AA;
 SQ
 Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGTCLVIFVTLVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGTCLVIFVTLVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDNDDESNMPCWQVKQLRQLVRKWLRTSEETISTVQEKQONISPLVRRGPQ 120
 DB 61 DDSYWDNDDESNMPCWQVKQLRQLVRKWLRTSEETISTVQEKQONISPLVRRGPQ 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDPDPILLMKSARNCSWDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDPDPILLMKSARNCSWDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

```

RESULT 5
AAW56760
ID AAW56760 standard; protein; 281 AA.
XX
AC AAW56760;
XX
DT 05-AUG-1998 (first entry)
XX
DE Human TRAIL polypeptide.
XX
KW Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
KW cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..18
FT /note= "N-terminal cytoplasmic domain"
FT Region 19..38
FT /note= "transmembrane region"
FT Domain 39..281
FT /note= "extracellular domain"
XX
XX US5763223-A.
XX
XX 09-JUN-1998.
XX
XX 25-JUN-1996; 96US-00670354.
XX
XX 29-JUN-1995; 95US-00496632.
XX
XX 01-NOV-1995; 95US-00548368.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Goodwin RG, Wiley SR;
XX
XX WPI; 1998-347322/30.
XX
XX N-PSDB; AAV29518.
XX
XX DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful
XX for producing recombinant polypeptides for research and therapy of
XX leukaemia, lymphoma, melanoma and viral infections.
XX
XX Claim 1; Col 33-36; 28pp; English.
XX
XX This represents a human tumour necrosis factor related apoptosis ligand
XX (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce
XX apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful
XX for producing the recombinant TRAIL polypeptides, which may be useful in
XX studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
XX (e.g. to isolate antigens for vaccine development). The polypeptides can
XX be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
XX treatment of blood or bone-marrow), or to treat viral infections
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MAMVEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMVEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYDPNDESNMSPQWQVQLRQLVRKWLRTSEETISTVQEKQNIPLVRERGPO 120
DB 61 DDSYDPNDESNMSPQWQVQLRQLVRKWLRTSEETISTVQEKQNIPLVRERGPO 120
QY 121 RVAAHITGTRNTLSSPNKNEKALGRKINSWESSRSGHSLNLHLNGLVITHEKG 180
DB 121 RVAAHITGTRNTLSSPNKNEKALGRKINSWESSRSGHSLNLHLNGLVITHEKG 180

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QY 181 FYIYSQTYFRQEIEIKENTKNDKQMVQIYKYTSYDPDPILLMKSNCSWSDAEYGLY 240
DB 181 FYIYSQTYFRQEIEIKENTKNDKQMVQIYKYTSYDPDPILLMKSNCSWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281

RESULT 6
AAW44354
ID AAW44354 standard; protein; 281 AA.
XX
AC AAW44354;
XX
DT 28-MAY-1998 (first entry)
XX
DE Human AGP-1.
XX
KW Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
KW bone resorption; haematopoietic disease.
XX
OS Homo sapiens.
XX
XX WO9746686-A2.
XX
XX 11-DEC-1997.
XX
XX 06-JUN-1997; 97WO-US009895.
XX
XX 07-JUN-1996; 96US-00660562.
XX
XX (AMGE-) AMGEN INC.
XX
XX Johnson MJ, Simonet WS, Danilenko DM;
XX WPI; 1998-042194/04.
XX
XX N-PSDB; AAV15295.
XX
XX Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -
XX useful for treating inflammation, bone resorption and haematopoietic
XX diseases.
XX
XX Claim 7; Page 36-37; 54pp; English.
XX
XX The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
XX factor (TNF)-related protein, involved in inflammation, myelopoiesis and
XX bone resorption. It has the same nucleic acid and amino acid (aa)
XX sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
XX in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
XX reagents for detecting AGP-1 expression. Nucleic acid complementary to
XX AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
XX used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
XX erythematosus, psoriasis, scleroderma, infection-related inflammation) or
XX bone resorption diseases (e.g. osteoporosis, osteomyelitis,
XX hypercalcaemia, Paget's disease). AGP-1 can be used to treat
XX haematopoietic diseases associated with reduction in the number of bone
XX marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
XX by disease, injury or exposure to myelosuppressive agents. Host cells,
XX transformed with expression vectors containing AGP-1 DNA, are used to
XX produce recombinant AGP-1
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MAMVEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMVEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60

```


QY 61 DDSYDPNDESNPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DDSYDPNDESNPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQVYIYKYTSYPDPILLMKSARNSCWSDAEYGLY 240
 DB 181 FYIYSQTYFRFOEEIKENTKNDKQWQVYIYKYTSYPDPILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7
 AAY01517
 ID AAY01517 standard; peptide; 281 AA.
 AC AAY01517;
 DT 27-MAY-1999 (first entry)
 DE Protein associated with neurodegenerative and autoimmune diseases.
 DE Neurodegenerative disease; autoimmune disease; inflammatory disease;
 KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
 KW surface receptor; TRAIL protein.
 OS Homo sapiens.
 XX FR2766713-A1.
 PN 05-FEB-1999.
 PD 04-AUG-1997; 97FR-00010176.
 PF 04-AUG-1997; 97FR-00010176.
 PR (INMR) BIO MERIEUX.
 PA Rieger F, Belliveau JF, Perron H;
 PI WPI; 1999-156177/14.
 DR Use of polypeptide derived from TRAIL protein for diagnosis of
 PT degenerative disease - autoimmunity and inflammation, also useful in
 PT prevention or treatment, and similar use of corresponding ligand and
 PT nucleic acid.
 XX Claim 2; Page 13; 21pp; French.
 XX The specification describes the use a polypeptide corresponding to at
 CC least the primary sequence of part of the present sequence to produce a
 CC diagnostic, prophylactic or therapeutic composition useful in cases of
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
 CC be used in treatment of neurodegenerative disease, lupus erythematosus,
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
 CC nervous system cells, antigenic and specifically recognise the surface
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
 CC receptors, inhibiting formation of natural complex
 XX Sequence 281 AA;
 SQ Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60
 DB 61 DDSYDPNDESNPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQVYIYKYTSYPDPILLMKSARNSCWSDAEYGLY 240
 DB 181 FYIYSQTYFRFOEEIKENTKNDKQWQVYIYKYTSYPDPILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8
 AAY27012
 ID AAY27012 standard; protein; 281 AA.
 AC AAY27012;
 DT 24-SEP-1999 (first entry)
 DE Human Apo-2 ligand (Apo-2L) polypeptide.
 DE Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
 KW lupus; immune-mediated glomerular nephritis; human.
 OS Homo sapiens.
 XX WO9936535-A1.
 PN 22-JUL-1999.
 PD 15-JAN-1999; 99WO-US001039.
 PF 15-JAN-1998; 98US-00007886.
 PR 15-APR-1998; 98US-00060533.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;
 PI WPI; 1999-444397/37.
 DR N-PSDB; AAX86987.
 XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 PT in mammalian cancer cells.
 PT Claim 1; Fig 1A; 86pp; English.
 XX This sequence represents a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis
 XX Sequence 281 AA;
 SQ Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60

QY 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60
Db |||||
1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVKWQLRQLVKRMILRTSEETISTVQEKQONISPLVRERGPO 120
Db |||||
61 DSYWDPNDEESMNSPCWQVKWQLRQLVKRMILRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180
Db |||||
121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180
QY 181 FYYIYSQTYFRFOEBIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNSCWSKDAEYGLY 240
Db |||||
181 FYYIYSQTYFRFOEBIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db |||||
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 9
AA181956
ID AAY81956 standard; protein; 281 AA.
XX
AC AAY81956;
DT 10-JUL-2000 (first entry)
DE Human Apo-2 ligand protein sequence.
DE
KW Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
KW therapy; apoptosis; cancer.
XX
OS Homo sapiens.
XX
PN US6046048-A.
XX
PD 04-APR-2000.
XX
PF 08-JAN-1997; 97US-00780496.
XX
PR 09-JAN-1996; 96US-0009755P.
XX
PA (GETH) GENENTECH INC.
PI Kim KJ, Ashkenazi AJ, Chuntharapai A;
XX
DR WPI; 2000-282690/24.
DR N-PSDB; AAA07425.
XX
PT New isolated monoclonal antibodies having antigen specificity for Apo-2
PT ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo
PT -2 ligand serum, and for treating diseases associated with increased
PT apoptosis.
XX
PS Claim 9; Fig 1a; 46pp; English.
XX
CC This sequence is the human Apo-2 ligand protein, which is recognised by
CC monoclonal antibodies produced by the hybridoma cell lines of the
CC invention. The hybridoma cell lines are deposited under the American Type
CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
CC tissues, or serum. The antibodies may also be employed as therapeutics.
CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
CC pathological conditions or diseases associated with increased apoptosis.
CC They are also useful for the affinity purification of Apo-2 ligand from
CC recombinant cell culture or natural sources. The Apo-2 ligand itself may
CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60
Db |||||
1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVKWQLRQLVKRMILRTSEETISTVQEKQONISPLVRERGPO 120
Db |||||
61 DSYWDPNDEESMNSPCWQVKWQLRQLVKRMILRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180
Db |||||
121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180
QY 181 FYYIYSQTYFRFOEBIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNSCWSKDAEYGLY 240
Db |||||
181 FYYIYSQTYFRFOEBIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db |||||
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 10
AAB24038
ID AAB24038 standard; protein; 281 AA.
XX
AC AAB24038;
DT 25-JAN-2001 (first entry)
XX
DE Human PRO1096 protein sequence SEQ ID NO:51.
XX
KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
KW identification; tumourigenesis; anticancer; detection.
XX
OS Homo sapiens.
XX
PN WO2000053750-A1.
XX
PD 14-SEP-2000.
XX
PF 02-DEC-1999; 99WO-US028551.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
XX
DR WPI; 2000-594320/56.
DR N-PSDB; AAC58120.
XX
PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit
PT the growth of tumors in mammals, and to identify inhibitors of PRO
PT polypeptide activity or expression.
XX
PS Claim 61; Fig 36; 226pp; English.
XX
CC The present invention describes an antibody that binds to a human protein
CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
CC activity and can be used to diagnose tumours in mammals, by detecting
CC complex formation when the antibody is contacted with test cells.
CC Increased expression of genes encoding (I) can also be detected to

CC diagnose tumours. Agents which inhibit the activity of (I), especially
 CC the antibodies, or an antisense oligonucleotide which hybridizes to genes
 CC encoding (I), can be used to inhibit tumour growth, preferably by
 CC inducing cell death. Methods from the present invention can be used to
 CC identify compounds which inhibit the biological activity of (I). AAC58019
 CC to AAC58102 represent PCR primers and hybridisation probes used in
 CC examples from the present invention for human PRO sequences. AAC58103 to
 CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
 CC protein sequences given in the exemplification of the present invention
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDNDDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DDSYWDNDDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281

RESULT 11

AAB08545
 ID AAB08545 standard; protein; 281 AA.

XX AAB08545;

DT 20-DEC-2000 (first entry)

DE Amino acid sequence of a human TRAIL polypeptide.

XX Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;
 KW TNF related apoptosis-inducing ligand; tumour cell;
 KW TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;
 KW non-small cell lung carcinoma.

XX Homo sapiens.

XX WO200048619-A1.

XX 24-AUG-2000.

XX 15-FEB-2000; 2000WO-US003891.

XX 16-FEB-1999; 99US-0120313P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Rosen GD;

XX WPI; 2000-558253/51.

XX N-PSDB; AAA64325.

XX Killing of tumor cells, e.g. solid tumors or carcinoma, comprises
 PT administration of synergistic combination of diterpenoid diepoxide and
 PT tumor necrosis factor related apoptosis-inducing ligand.

XX

PS Disclosure; Page 23-24; 29pp; English.

XX The present sequence represents a human TRAIL (tumour necrosis factor
 CC (TNF) related apoptosis-inducing ligand) polypeptide. The specification
 CC describes a method for enhanced killing of tumour cells. The method
 CC comprises contacting a susceptible tumour cell with a synergistic mixture
 CC of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined
 CC dosage to kill at least 50 % of the cells. This mixture is synergistic,
 CC and so is active at lower doses and against otherwise resistant cell
 CC lines. The method is used for killing tumour cells, especially solid
 CC tumours or carcinomas (especially mammary carcinoma or non-small cell
 CC lung carcinoma)

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDNDDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DDSYWDNDDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281

RESULT 12

AAB28691

ID AAB28691 standard; protein; 281 AA.

XX AAB28691;

DT 14-FEB-2001 (first entry)

DE Human AGP-1.

KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
 KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
 KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
 KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
 KW transplant rejection; cardiovascular disease; arteriosclerosis.

XX Homo sapiens.

XX WO200063253-A1.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008004.

XX 16-APR-1999; 99US-00293245.

XX (AMGE-) AMGEN INC.

XX Hsu H, Meng S;

XX WPI; 2000-665240/64.

XX N-PSDB; AAC67831.

XX AAB67243;
 AC 19-APR-2001 (first entry)
 DT XX
 XX Human Apo2 ligand.
 DE XX
 XX Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
 KW XX
 XX Homo sapiens.
 OS XX
 XX WO200100832-A1.
 PN XX
 XX 04-JAN-2001.
 PD XX
 XX 26-JUN-2000; 2000WO-US017579.
 PF XX
 XX 28-JUN-1999; 99US-0141342P.
 PR XX
 XX (GETH) GENENTECH INC.
 PA XX
 XX Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
 PI O'Connell M, Pai R, Shahrokh Z, Simmons L;
 PI XX
 XX WPI; 2001-123012/13.
 DR XX
 XX Use of divalent metal ions for making Apo-2 ligand and in formulations
 PT containing Apo-2 ligand for increasing yield and stability of ligand
 PT trimers, useful for therapeutic applications.
 PT XX
 XX Claim 6; Fig 1; 60pp; English.
 PS XX
 XX The present invention relates to a formulation comprising Apo-2 ligand
 CC and divalent metal ions. Apo-2 ligand and the formulation are useful for
 CC treating cancers and viral infections. Addition of divalent metal ions
 CC for making Apo-2 ligand and formulations containing Apo-2 ligand results
 CC in increased yield and stability of Apo-2 ligand trimers
 CC XX
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 1478; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDEESNNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
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 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVIEHGK 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVIEHGK 180
 QY 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEGLY 240
 DB 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHMDHEASFFGAFLVG 281

RESULT 15
 AAEL1031
 ID AAEL1031 standard; protein; 281 AA.
 XX
 AC AAEL1031;
 XX
 XX 18-DEC-2001 (first entry)
 DT XX
 XX

DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
 XX
 KW Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
 KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
 KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
 KW melanoma.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..18
 FT /label= N_terminal_cytoplasmic_domain
 FT Region 19..38
 FT /label= Transmembrane_region
 FT Domain 39..281
 FT /label= Extracellular_domain
 XX
 PN US6284236-B1.
 XX
 PD 04-SEP-2001.
 XX
 XX 26-MAY-1999; 99US-00320424.
 PF XX
 XX 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548368.
 PR 25-JUN-1996; 96US-00670354.
 PR 26-MAR-1998; 98US-00048641.
 PR 10-NOV-1998; 98US-00190046.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 XX Wiley SR, Goodwin RG;
 PI
 XX WPI; 2001-595463/67.
 DR N-PSDB; AAD18395.
 XX
 XX New tumor necrosis factor related apoptosis inducing ligand polypeptides
 PT for treating viral infections (e.g. bovine viral diarrhoea or human
 PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
 PT XX
 XX Claim 2; Col 45-48; 41pp; English.
 PS
 XX The invention relates to a cytokine designated as tumour necrosis factor
 CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
 CC of certain target cells, including cancer cells and virally infected
 CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
 CC treating viral infections (e.g. bovine viral diarrhoea or human
 CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
 CC melanoma), as a research reagent useful in studying apoptosis including
 CC the regulation of programmed cell death. TRAIL DNA sequences may be
 CC employed in developing a gene therapy approach to treating disorders
 CC mediated by defective or insufficient amounts of TRAIL, in the production
 CC of TRAIL polypeptides and as probes or primers in polymerase chain
 CC reactions (PCR). The present sequence is human TRAIL protein
 CC XX
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 1478; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDEESNNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DDSYWDPNDEESNNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVIEHGK 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVIEHGK 180

Qy 181 FYYISQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYYISQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

Search completed: June 22, 2005, 06:07:13
Job time : 128.948 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:01:21 ; Search time 652.628 Seconds

(without alignments)
165.329 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMEVQGSFSLGCTCLIV.....NEHLIDMDHEASFFGAFLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1478	100.0	281	8	US-08-916-625B-6
2	1478	100.0	281	8	US-08-971-317A-8
3	1478	100.0	281	9	US-09-813-329-17
4	1478	100.0	281	9	US-09-193-663-8
5	1478	100.0	281	9	US-09-934-465-1
6	1478	100.0	281	10	US-09-919-039-118
7	1478	100.0	281	13	US-10-011-125-4
8	1478	100.0	281	13	US-10-001-054-54
9	1478	100.0	281	14	US-10-093-766-54
10	1478	100.0	281	14	US-10-174-654-11
11	1478	100.0	281	14	US-10-151-882-41

12	1478	100.0	281	14	US-10-218-547-20
13	1478	100.0	281	14	US-10-322-673-72
14	1478	100.0	281	14	US-10-139-785-66
15	1478	100.0	281	14	US-10-310-793-26
16	1478	100.0	281	15	US-10-279-687-8
17	1478	100.0	281	15	US-10-292-486-5
18	1478	100.0	281	15	US-10-333-713-1
19	1478	100.0	281	15	US-10-662-429-2
20	1478	100.0	281	15	US-10-202-062-20
21	1478	100.0	281	15	US-10-662-431-2
22	1478	100.0	281	15	US-10-662-430-2
23	1478	100.0	281	15	US-10-652-244-2
24	1478	100.0	281	16	US-10-381-160-5
25	1478	100.0	281	16	US-10-755-889-210
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28	1478	100.0	281	16	US-10-825-282-22
29	1478	100.0	281	16	US-10-825-282-24
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31	1478	100.0	281	16	US-10-688-845-36
32	1478	100.0	281	16	US-10-861-685-1
33	1478	100.0	281	17	US-10-771-254-1
34	1478	100.0	281	17	US-10-855-559-2
35	1478	100.0	281	17	US-10-451-200-5
36	1478	100.0	281	17	US-10-495-353-1
37	1478	100.0	281	17	US-10-652-973-1
38	1469	99.4	279	13	US-10-066-209-3
39	1456	98.5	279	16	US-10-367-094-22
40	1437	97.2	283	17	US-10-978-203-23
41	1437	97.2	283	17	US-10-978-131-23
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45	1017	68.8	208	9	US-09-855-544A-16

ALIGNMENTS

RESULT 1.

US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Publication NO. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; TITLE OF INVENTION: RECEPTOR, TR6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-50008-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-916-625B-6

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60
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DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 2

US-08-971-317A-8
Sequence 8, Application US/08971317A
Publication No. US20010010925A1
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,317A
FILING DATE: 17-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Goller, Mimi C
REGISTRATION NUMBER: 39,046
REFERENCE/DOCKET NUMBER: 6255.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550

TELEFAX: (847) 938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-8

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60
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DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 3

US-09-813-329-17
Sequence 17, Application US/09813329
Patent No. US20020012968A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.jp
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 281
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-813-329-17

Query Match 100.0%; Score 1478; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 FYIYISQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYISQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 4

US-09-193-663-8
; Sequence 8, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255, US. 02
; CURRENT APPLICATION NUMBER: US/09/193,663
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-8

Query Match 100.0%; Score 1478; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 DDSYDNDPEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
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QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 5

US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669,22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match 100.0%; Score 1478; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYYFTNELKQMDKYKSGIACFLKE 60
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Db 61 DDSYDNDPEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
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Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVTHEKG 180
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Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 6

US-09-919-039-118
; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118

Query Match 100.0%; Score 1478; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYDNDPEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYDNDPEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVTHEKG 180
QY 181 FYIYISQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYISQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

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RESULT 7
US-10-011-125-4
; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4
Query Match 100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128; Indels 0; Gaps 0;
Matches 281; Conservative 0; Mismatches 0;
QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
QY 61 DSYWDPNDEESNNSPCWQVKQQLRQLVRKMLIRTSEETISTVQEKQQNISPLVRERGQ 120
Db 61 DSYWDPNDEESNNSPCWQVKQQLRQLVRKMLIRTSEETISTVQEKQQNISPLVRERGQ 120
QY 121 RVAAHITGTGRSNTLSSNPKKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
Db 121 RVAAHITGTGRSNTLSSNPKKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
QY 181 FYYISQTYFRQEEIKENTKDKQWQVIYKYTSYPDPILLMKSNRSCWKSDAEYGLY 240
Db 181 FYYISQTYFRQEEIKENTKDKQWQVIYKYTSYPDPILLMKSNRSCWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281

RESULT 8
US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Shelton, David
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/082999
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; PRIOR APPLICATION NUMBER: 60/083545
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; PRIOR APPLICATION NUMBER: 60/144758
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; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/187202
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;; PRIOR APPLICATION NUMBER: 09/709238
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 09/802706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 09/866034
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 09/872035
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;; PRIOR FILING DATE: 2001-06-14
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;; PRIOR FILING DATE: 2001-07-30
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;; PRIOR FILING DATE: 2001-08-06
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;; PRIOR APPLICATION NUMBER: PCT/US99/08615
;; PRIOR FILING DATE: 1999-04-20
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;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28551
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;; PRIOR APPLICATION NUMBER: PCT/US99/28634
;; PRIOR FILING DATE: 1999-12-01
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;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00376
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;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: PCT/US00/04341
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/04342
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: PCT/US00/06884
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;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: PCT/US00/14941
;; PRIOR FILING DATE: 2000-05-30
;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US00/22031
;; PRIOR FILING DATE: 2000-08-11
;; PRIOR APPLICATION NUMBER: PCT/US00/23522
;; PRIOR FILING DATE: 2000-08-23
;; PRIOR APPLICATION NUMBER: PCT/US00/30873

;; PRIOR FILING DATE: 2000-11-10
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: PCT/US01/06666
;; PRIOR FILING DATE: 2001-03-01
;; PRIOR APPLICATION NUMBER: PCT/US01/17092
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: PCT/US01/17800
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; PRIOR APPLICATION NUMBER: PCT/US01/27099
;; PRIOR FILING DATE: 2001-08-29
;; NUMBER OF SEQ ID NOS: 91
;; SEQ ID NO 54
;; LENGTH: 281
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-001-054-54

Query Match 100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKGIACFLKE 60
|||
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKGIACFLKE 60
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QY 61 DDSYWDPNDEESNNSPCWQVKQLRVKMLRTSEETISTVQEKQONISPLVRERGQ 120
|||
Db 61 DDSYWDPNDEESNNSPCWQVKQLRVKMLRTSEETISTVQEKQONISPLVRERGQ 120
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QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180
|||
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180
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QY 181 FYYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
|||
Db 181 FYYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
|||
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
|||
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
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RESULT 9
US-10-093-766-54
; Sequence 54, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60

QY 61 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMLILRTSEETISTVQEQQNISPLVRERGPO 120
DB 61 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMLILRTSEETISTVQEQQNISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180

QY 181 FYIYSQTYFRQOEIKENTKNDKQMVQYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240
DB 181 FYIYSQTYFRQOEIKENTKNDKQMVQYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLV 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLV 281

RESULT 10
US-10-174-654-11
; Sequence 11, Application US/10174654
; Publication No. US20030044937A1
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; Jones, Cynthia J
; Mills, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/174,654
; FILING DATE: 19-Jun-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-174-654-11

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;

RESULT 12
US-10-218-547-20
; Sequence 20, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:

Query Match	100.00%;	Score 1478;	DB 14;	Length 281;
Best Local Similarity	100.00%;	Pred. No. 1.5e-128;		
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Db	1	MAMMEVGGGSPSLGQTCVLIVIFVTLVLSQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE	60
Qy	61	DDSYWDPNDEESMNSPCWQVKWLRLVRKMLRTSEETISTVQEKQONISPLVRERGPO	120
Db	61	DDSYWDPNDEESMNSPCWQVKWLRLVRKMLRTSEETISTVQEKQONISPLVRERGPO	120
Qy	121	RVAAHITGTRGRSNTVSSPNSKNEKALGRKINSWESSRSGHSPLSLHLRNGELVITHKG	180
Db	121	RVAAHITGTRGRSNTVSSPNSKNEKALGRKINSWESSRSGHSPLSLHLRNGELVITHKG	180
Qy	181	FYIYSQTFRFOEIEKENTKNDKQWQVYIYKTSYDPDPLLMKSARNCSWSDAEVGLY	240
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Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG	281
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG	281

RESULT 14

US-10-139-785-66

; Sequence 66, Application US/10139785

; Publication No. US20030190685A1

; GENERAL INFORMATION:

; APPLICANT: Salcedo et al.

; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to TRAIL

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: PF550

; CURRENT APPLICATION NUMBER: US/10/139,785

; CURRENT FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: 60/369,960

; PRIOR FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: 60/341,237

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: 60/331,310

; PRIOR FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/331,044

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: 60/327,364

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/323,807

; PRIOR FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: 60/309,176

; PRIOR FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: 60/294,981

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/293,473

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 66

; LENGTH: 281

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-139-785-66

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Best Local Similarity	100.00%;	Pred. No. 1.5e-128;		
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Db	1	MAMMEVGGGSPSLGQTCVLIVIFVTLVLSQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE	60
Qy	61	DDSYWDPNDEESMNSPCWQVKWLRLVRKMLRTSEETISTVQEKQONISPLVRERGPO	120
Db	61	DDSYWDPNDEESMNSPCWQVKWLRLVRKMLRTSEETISTVQEKQONISPLVRERGPO	120

121	RVA	AHIT	TG	RS	NT	LS	SP	SK	NE	K	AL	G	R	K	I	N	S	W	E	S	S	R	G	H	S	F	L	N	L	H	L	R	G	E	L	V	I	T	H	E	K	G	180									
121	RVA	AHIT	TG	RS	NT	LS	SP	SK	NE	K	AL	G	R	K	I	N	S	W	E	S	S	R	G	H	S	F	L	N	L	H	L	R	G	E	L	V	I	T	H	E	K	G	180									
181	FY	I	S	Q	T	Y	R	F	O	E	I	K	E	N	T	K	N	D	K	M	Q	W	Y	I	K	Y	T	S	P	D	P	I	L	L	M	K	S	A	R	N	S	C	S	K	D	A	E	Y	G	L	Y	240
181	FY	I	S	Q	T	Y	R	F	O	E	I	K	E	N	T	K	N	D	K	M	Q	W	Y	I	K	Y	T	S	P	D	P	I	L	L	M	K	S	A	R	N	S	C	S	K	D	A	E	Y	G	L	Y	240
241	SI	Y	O	G	I	P	E	L	K	E	N	D	R	I	F	V	S	T	N	E	H	L	I	D	M	D	H	E	A	S	P	F	G	A	F	L	V	G	281													
241	SI	Y	O	G	I	P	E	L	K	E	N	D	R	I	F	V	S	T	N	E	H	L	I	D	M	D	H	E	A	S	P	F	G	A	F	L	V	G	281													

Search completed: June 22, 2005, 06:39:13
Job time : 653.628 secs

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RESULT 15
US-10-310-793-26
; Sequence 26, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wai, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; RELATING TO HUMAN TUMOR NECROSIS FACTOR-GAMMA BETA
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-310-793-26

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	Query Match	100.0%	Score 1478;	DB 14;	Length 281;
	Best Local Similarity	100.0%	Pred. No. 1.5e-128;		
	Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAMMEVGGPSLGGTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE	60		
Db	1	MAMMEVGGPSLGGTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSKSGIACFLKE	60		
Qy	61	DDSYWDNDNDESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQP	120		
Db	61	DDSYWDNDNDESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQP	120		
Qy	121	RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFISLNLHRLNGELVIEHKG	180		
Db	121	RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFISLNLHRLNGELVIEHKG	180		

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 32.1756 Seconds
(without alignments)
651.935 Million cell updates/sec

Title: US-10-662-429-2
Perfect score: 1478
Sequence: 1- MAMMEVQGSPSLGQTCVLIV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	1	US-08-670-354-2
2	1478	100.0	281	3	US-08-584-031-1
3	1478	100.0	281	3	US-08-780-496-1
4	1478	100.0	281	3	US-08-883-086-10
5	1478	100.0	281	3	US-09-320-424-2
6	1478	100.0	281	3	US-09-333-593A-6
7	1478	100.0	281	4	US-09-157-864-11
8	1478	100.0	281	4	US-09-825-563-2
9	1478	100.0	281	4	US-09-919-039-118
10	1478	100.0	281	4	US-09-582-450-1
11	1478	100.0	281	4	US-09-934-465-1
12	1478	100.0	281	4	US-10-011-125A-4
13	1478	100.0	281	5	PCT-US96-10895-2
14	1469	99.4	279	3	US-09-072-993C-3
15	1238	83.8	271	4	US-09-569-611C-30
16	988	66.8	253	3	US-09-320-424-11
17	988	66.8	253	4	US-09-825-563-11
18	988	66.8	256	3	US-09-320-424-13
19	988	66.8	256	4	US-09-825-563-13
20	930	62.9	177	3	US-09-105-343A-7
21	930	62.9	291	1	US-08-670-354-6
22	930	62.9	291	3	US-09-320-424-6
23	930	62.9	291	4	US-09-825-563-6
24	930	62.9	291	5	PCT-US96-10895-6
25	850	57.5	161	4	US-09-565-423-7
26	735	49.7	169	4	US-09-569-611C-29
27	654	44.2	183	3	US-09-105-343A-8

28	611	41.3	121	4	US-09-513-999C-7833	Sequence 7833, Ap
29	483	32.7	120	4	US-08-569-611C-32	Sequence 32, Appl
30	482	32.6	101	1	US-08-670-354-4	Sequence 4, Appl
31	482	32.6	101	3	US-09-320-424-4	Sequence 4, Appl
32	482	32.6	101	4	US-09-825-563-4	Sequence 4, Appl
33	482	32.6	101	5	PCT-US96-10895-4	Sequence 4, Appl
34	482	32.6	122	4	US-09-569-611C-31	Sequence 31, Appl
35	446	30.2	85	4	US-09-632-287A-12	Sequence 12, Appl
36	258.5	17.5	294	3	US-08-996-139-11	Sequence 11, Appl
37	258.5	17.5	294	3	US-08-995-659-11	Sequence 11, Appl
38	258.5	17.5	294	3	US-09-215-649A-11	Sequence 11, Appl
39	258.5	17.5	294	4	US-09-577-780-11	Sequence 11, Appl
40	258.5	17.5	294	4	US-09-577-800-11	Sequence 11, Appl
41	258.5	17.5	294	4	US-09-466-496-11	Sequence 11, Appl
42	258.5	17.5	294	4	US-09-871-856-11	Sequence 11, Appl
43	258.5	17.5	294	4	US-09-871-291-11	Sequence 11, Appl
44	258.5	17.5	294	4	US-09-877-650-11	Sequence 11, Appl
45	258.5	17.5	294	4	US-09-865-363-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

Query Match 100.0%; Score 1478; DB 1; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180

QY 181 FYIYSQTYFRFOEEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 2

US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584, 031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60
DB 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180

QY 181 FYIYSQTYFRFOEEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 3

US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim

; TITLE OF INVENTION: Apo-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-780-496-1

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60
DB 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180

QY 181 FYIYSQTYFRFOEEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 4

US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA


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; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134, US. 01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
; US-08-883-086-10

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYWDPNDEESNMPQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESNMPQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

Qy 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
Db 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180

Qy 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 6
US-09-333-593A-6
; Sequence 6, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 281
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-333-593A-6

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYWDPNDEESNMPQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDPNDEESNMPQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

Qy 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
Db 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180

Qy 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 5
US-09-320-424-2
; Sequence 2, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,369
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; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
US-09-919-039-118

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLANGELVIEHGK 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLANGELVIEHGK 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 11
US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. 6746668
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60
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DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLANGELVIEHGK 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLANGELVIEHGK 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 12
US-10-011-125A-4
; Sequence 4, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
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; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
US-09-919-039-118

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLANGELVIEHGK 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLANGELVIEHGK 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 10
US-09-582-450-1
; Sequence 1, Application US/09582450
; Patent No. 6740739
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Kelley, Robert F.
; APPLICANT: O'Connell, Mark P.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Schwall, Ralph H.
; TITLE OF INVENTION: APO-2 Ligand
; FILE REFERENCE: P0978P4
; CURRENT APPLICATION NUMBER: US/09/582,450
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/007,886
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 09/060,533
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-450-1

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US96-10895-2
; US-10-011-125A-4

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEQGPGSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMVEQGPGSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DSDYDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSDYDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180

QY 181 FYIYSQTYRFOEBIKENTKNDKQWQVYIYKYTSYDPDILLMKSARNCSWKDAEYGLY 240
Db 181 FYIYSQTYRFOEBIKENTKNDKQWQVYIYKYTSYDPDILLMKSARNCSWKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 13
PCT-US96-10895-2
; Sequence 2, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10895-2

Query Match 100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEQGPGSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMVEQGPGSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DSDYDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSDYDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180

QY 181 FYIYSQTYRFOEBIKENTKNDKQWQVYIYKYTSYDPDILLMKSARNCSWKDAEYGLY 240
Db 181 FYIYSQTYRFOEBIKENTKNDKQWQVYIYKYTSYDPDILLMKSARNCSWKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 14
US-09-072-993C-3
; Sequence 3, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-072-993C-3

Query Match 99.4%; Score 1469; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 3.1e-148;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKED 62
Db 1 MMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKED 60

QY 63 SYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 122

Db 61 SYWDPNDESMNPGCWKQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQRV 120
Qy 123 AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY 182
Db 121 AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY 180
Qy 183 YIYSQTYFRFOEIKENTKNDKQWQVYIYKYTSYPPDPILLMKSARNSCWSDAEYGLYSI 242
Db 181 YIYSQTYFRFOEIKENTKNDKQWQVYIYKYTSYPPDPILLMKSARNSCWSDAEYGLYSI 240
Qy 243 YOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 YOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279

RESULT 15

US-09-569-611C-30
; Sequence 30, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-30.

Query Match 83.8%; Score 1238; DB 4; Length 271;
Best Local Similarity 85.4%; Pred. No. 1.3e-123;
Matches 240; Conservative 2; Mismatches 5; Indels 34; Gaps 2;

Qy 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVTVYFTNELKQMDKYKSGIACFLKE 60
Db 25 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVTVYFTNELKQMDKYKSGIACFLKE 84
Qy 61 DDSYWDPNDESMNPGCWKQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 85 DDSYWDPNDESMNPGCWKQKQLRQLVRK-----KSNKIFLPLVRERGPQ 130
Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 131 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 190
Qy 181 FYIYSQTYFRFOEIKENTKNDKQWQVYIYKYTSYPPDPILLMKSARNSCWSDAEYGLY 240
Db 191 FYIYSQTYFRFOEIKENTKNDKQWQVYIYKYTSYPPDPILLMKSARNSCWSDAEYGLY 250
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 251 SIYQG-----IDMDHEASFFGAFLVG 271

Search completed: June 22, 2005, 06:02:15
Job time : 33.1756 secs

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R:Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A>Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A:Reference number: JC2340; MUID:95071350; PMID:7980502
A:Accession: JC2340
A:Molecule type: DNA
A:Residues: 1-281 <MIT>
A:Cross-references: GB:D38122; DDBJ:D29820; NID:G601892; PIDN:BAA07320.1; PID:gl369902
R:Schatzlein, C.B.
A:Reference number: S57565
A:Accession: S57565
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-281 <SCH>
A:Cross-references: EMBL:X89102; NID:G887455; PID:G887456
R:Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G.J. Exp. Med. 181, 71-77, 1995
A>Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A:Reference number: I38554; MUID:95105731; PMID:7528780
A:Accession: I38554
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-281 <RE2>
A:Cross-references: EMBL:U08137; NID:G624627; PIDN:AAC50071.1; PID:G624628
C:Genetics:
A:Gene: FasL
A:Introns: 151/1; 116/3
A:Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.2%; Score 182.5; DB 2; Length 281;
Best Local Similarity 27.4%; Pred. No. 4.8e-08;
Matches 57; Conservative 40; Mismatches 70; Indels 41; Gaps 10;

QY 44 WQLRQLVRKMI-LRTSEETISTVQEKQNI---SPLVRERGPORVAAHITGTRGRSNTLS 99
Db 102 FQLFLHQLKELAELESTSQMHTASSLEKQIGHSP-PPEKKELRKVAHLT---GKSNRS 157
QY 100 SPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKGFYIYQTYRFOEIK 159
Db 158 MP-----LEWEDT-YGIVLLSGVKYKGGVLINETGLYFYVKVYFRGQ---- 200
QY 160 ENTNDKQMVQYI-KYTSYPPDILLMKASRNS---CWSKDAEYGLYSYOGGIFEL 212
Db 201 --SCNLPISLHKVYMRNSKYQDLVMEGKMSYCTTGQWAR-----SSVLGAVFNL 251
QY 213 KENDRIFSVTNEHLIDMDHEASFFGAP 240
Db 252 TSADHLVNVSELSLVNFESQTFFGLY 279

RESULT 3
A49266
fas ligand - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: A49266
R:Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A>Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor gene family.
A:Reference number: A49266; MUID:94084792; PMID:7505205
A:Accession: A49266
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-278 <SUD>
A:Cross-references: UNIPROT:P36940; GB:U03470; NID:G440178; PIDN:AAC52129.1; PID:G440179
C:Keywords: glycoprotein; transmembrane protein

Query Match 13.8%; Score 177.5; DB 2; Length 278;
Best Local Similarity 27.5%; Pred. No. 1.3e-07;
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

QY 62 ISTVQEKQNI-SPLVRERGPORVAAHITGTRGRSNTLS-SPNSKNEKALGRKINSWESSR 120
Db 121 VSSFQKQIANPSTPSETKKPRSV-AHLTGNPSRSIPL-----EWEDT- 162
QY 121 SGHSFLSNLHLRNGELVHEKGFYIYQTYRFOEIKENTKNDKQMVQYIY-KYTSYP 179
Db 163 YGTALISGVKYGKGGVLINAEGLYFYVKVYFRGQ-----SCNSQPLSHKVMYMRNFKYP 216
QY 180 DPILLMKASR-NSCWSKDAEYGLYSYOGGIFELKENDRIFSVTNEHLIDMDHEASFFG 238
Db 217 GOLVLMEEKKLVNYCTT--GQIWAHSSYLGAVENTLVADHLVYNISQLSLINFESKTFPG 274
QY 239 AF 240
Db 275 LY 276

RESULT 4
S53090
CD40 ligand - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S53090
R:Wenters, B.E.L.C.; Muriuki, M.
A:Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A:Reference number: S53090
A:Accession: S53090
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <MER>
A:Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:G732569; PIDN:CAA88363.1; PID:G73257

Query Match 11.8%; Score 152; DB 2; Length 261;
Best Local Similarity 27.1%; Pred. No. 1.7e-05;
Matches 55; Conservative 39; Mismatches 77; Indels 32; Gaps 10;

QY 39 CMQVKWQLRQLVRKMLRTSEETISTVQEKQNI-SPLVRERGPORVAAHITGTRGRSNTL 98
Db 84 CHEIRSFPEDLV-KDIMQKE-----VKKKEKFNEMHKGQDEPQ-IAAHV-----I 127
QY 99 SPNSKNEKALGRKINSWESSRSGHSLN--LHLRNG-ELVHEKGFYIYQTYRFRQ 155
Db 128 SEASSKTTISVL-----QW--APKGYVTLNVLTLNGLKQLAVKRGQFYIYTVQVTFCSN 180
QY 156 EIKENTKNDKQMVQYIYKYTSYPPDILLMKASRNSCWSKDAEYGLYSYOGGIFELKEN 215
Db 181 RE-----TLGQAPFIASCLKSPSGSERILLRAANTHSSSKPC--GOOSIHLGSGVFELQSG 234
QY 216 DRIFSVTNEHLIDMDHEASFFG 238
Db 235 ASVFNVTDPQSQVSHGTGFTSFG 257

RESULT 5
S21738
CD40 ligand - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: S21738
R:Armstrong, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B.N.
Nature 357, 80-82, 1992
A>Title: Molecular and biological characterization of a murine ligand for CD40.
A:Reference number: S21738; MUID:92244364; PMID:1374165
A:Accession: S21738
A:Molecule type: mRNA
A:Residues: 1-260 <ARM>
A:Cross-references: UNIPROT:P27548; EMBL:X65453; NID:G50351; PIDN:CAA46448.1; PID:G50352
C:Keywords: glycoprotein; transmembrane protein
F;23-46/Domain: transmembrane #status predicted <TMM>
F;47-260/Domain: extracellular #status predicted <EXT>

F;239/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.8%; Score 138.5; DB 2; Length 260;
Best Local Similarity 25.1%; Pred. No. 0.00024;
Matches 47; Conservative 37; Mismatches 72; Indels 31; Gaps 8;
QY 39 CMQVKKQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGQORVAHAHITGTRGRSNTL 98
DB 84 CEEMRKQFQDLVKDITLTK-----EKKENSFEMQKQDQNFQ-IAAHV-----I 126
QY 99 SSPNSKNEKALGRKINSWESSRSGHSFLSNL--LHLRNG--ELVTHEKGFYIYSQTYFRFQ 156
DB 127 SEANSNAASVL-----QM--AKGYITMKSNLVLENGKQLTVKREGLYIYVTVTFCSNR 180
QY 157 EIKENTKNDKQMVQIYKYTSYPPDILLMKARNCSWKDAEYGLYSIYQGGIFELKEND 216
DB 181 E-----PSSQRPFTVGLWMLKPSIGSERILLKAAANTHSSQLCEQ--QSVHLGGVFELQAGA 234
QY 217 RIFVSVT 223
DB 235 SVFVNVT 241

RESULT 6

I53476
CD40 ligand - human
N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 09-Jul-2004
C;Accession: S28017; JH0793; S26694; S28852; I53476; S25584; S30593
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;
EMBO J. 11, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for
A;Reference number: S28017; MUID:93049181; PMID:1385114
A;Accession: S28017
A;Molecule type: mRNA
A;Residues: 1-261 <HOL>
A;Cross-references: UNIPROT:P29965; EMBL:Z15017; NID:G38483; PIDN:CAA78737.1; PID:G38484
R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
J. Exp. Med. 176, 1543-1550, 1992
A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin
A;Reference number: JH0793; MUID:9304757; PMID:1281209
A;Accession: JH0793
A;Molecule type: mRNA
A;Residues: 1-261 <SPR>
A;Cross-references: GB:X67878; NID:G38411; PIDN:CAA48077.1; PID:G38412
A;Experimental source: peripheral blood T-cell
R;Graf, D.; Korthauer U.; Mages, H.W.; Senger, G.; Kroczeck, R.A.
Eur. J. Immunol. 22, 3191-3194, 1992
A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A;Reference number: S26694; MUID:93076854; PMID:1280226
A;Accession: S26694
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <GRA>
A;Cross-references: EMBL:X68550; NID:G37269; PIDN:CAA48554.1; PID:G37270
R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
FEBS Lett. 315, 259-266, 1993
A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e
A;Reference number: S28852; MUID:93138085; PMID:7678552
A;Accession: S28852
A;Molecule type: mRNA
A;Residues: 1-261 <GAU>
A;Cross-references: EMBL:L07414; NID:G180123; PIDN:AAA35662.1; PID:G180124
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
C;Genetics:
A;Gene: GDB:CD40LG; HIGM1; IMD3
A;Cross-references: GDB:I120632; OMIM:308230
A;Map position: Xq26-Xq26
C;Keywords: glycoprotein; transmembrane protein
F;13-44/Domain: transmembrane #status predicted <TMM>
F;45-261/Domain: extracellular #status predicted <EXT>
F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.6%; Score 137; DB 2; Length 261;
Best Local Similarity 24.6%; Pred. No. 0.00033;
Matches 52; Conservative 38; Mismatches 73; Indels 48; Gaps 11;
QY 39 CMQVKKQLRQLVRKMLIRTSEETISTVQEKQONISPLVRERGQORVAHAHITGTRGRSNTL 98
DB 84 CBEIKSQFGFVKDML--NKEET-----KKENSFEMQKQDQNFQ-IAAHV-----I 127
QY 99 SSPNSKNEKALGRKINSWESSRSGHSFLSNL--LHLRNG--ELVTHEKGFYIYSQTYFRFQ 155
DB 128 SEASSKTSVL-----QM--ABKGYITMKSNNLVLENGKQLTVKROGLYIYIAQVTFCSN 180
QY 156 EIKENT-----KNDKQMVQIYKYTSYPPDILLMKARNCSWKDAEYGLYSIYQ 207
DB 181 REASSQAPFIASICKSPGRFER-----ILLRAANTHSSAKPC--GQOSIHLG 226
QY 208 GIFELKENDRIFVSVTNEHLIDMDHEASPF 238
DB 227 GVFEQFGASVFNVTDPQVSHGTGTFSG 257

RESULT 7

S17289
tumor necrosis factor beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: S17289
R;Kuhmert, P.; Wuehrlich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A;Reference number: S17289; MUID:91340150; PMID:1874444
A;Accession: S17289
A;Molecule type: DNA
A;Residues: 1-204 <KUH>
A;Cross-references: UNIPROT:P26445; EMBL:X54859; NID:G2132; PIDN:CAA38638.1; PID:G2133
C;Genetics:
A;Intons: 32/3; 68/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-204/Product: tumor necrosis factor beta #status predicted <MAT>
Query Match 10.5%; Score 134.5; DB 1; Length 204;
Best Local Similarity 24.7%; Pred. No. 0.00039;
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;
QY 63 STVQEKQONISPLVRERGQORVAHAHITG-----TRGRSNTLSSPNSKNEKALGRKINS 115
DB 42 SAAQPAHQH-PPKHLARGTLKPAAHLVGDPSTPDSLWRANT-----DRAPLR---- 88
QY 116 WESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKY 175
DB 89 -----HGFL-----LSNNSLLVPTSGLYFVYVQVFSGEGCFPKATPTPLYLAHEVQLF 137
QY 176 TS-YPPDILLMKARNCSWKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 234
DB 138 SSQYPPHVLPSAQKSCVCPQGPW-VRSVYQGAVELLTQGDQLSTHTDTPHLLSPSS 196
QY 235 SFFGAF 240
DB 197 VFFGAF 202
RESULT 8
A25451
tumor necrosis factor alpha precursor - rabbit
N;Alternate names: cachectin; TNF alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A25454; A25451; J50727
R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.
DNA 5, 149-156, 1986

Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;

QY 72 ISPLVNRGQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWE-----SSRSGH 123
Db 56 IGPQREKFPNNLP--IGSMAQTLLRSSSSQSSDKPVAHVAVNHQVDRQLEWLSRGAN 113

QY 124 SPLSN-LHLRNGELVTHEKGFYIYSQTYFRFOEIKENTKDKQVQYIYKY-TSPD 181
Db 114 ALLANGMDLKDQNLVLPADGLYIYQVLFKQ-----GCSSVLLTHTVSRFAVSYEDK 168

QY 182 ILLMKSARNCSWCKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLLDMDHEAS 235
Db 169 VNLLSAIKSPC-PKEITPEGSELKPWEPIYLGGVFQLEKGRDLSAEVNLPKYLDFAESGQ 227

QY 236 -PFG 238
Db 228 VFPG 231

RESULT 11
S24641
lymphotoxin - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: I46046; S24641
R:Cluets, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu
A:Reference number: I46046; MUID:94083525; PMID:8260599
A:Accession: I46046
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-204 <CL2>
A:Cross-references: UNIPROT:Q06600; EMBL:Z14137; NID:g796; PIDN:CAA78510.1; PID:g797
C:Genetics:
A:Introns: 32/3; 68/1
C:Superfamily: tumor necrosis factor

Query Match 9.9%; Score 127.5; DB 1; Length 204;
Best Local Similarity 24.9%; Pred. No. 0.0015;
Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 61 TISTVQEKQNISPLVRGQPVAAHITG-----TRGRSNTLSSPNSKNEKALGRKI 113
Db 40 TPSAAQPAHQQL-PTPTFTRGTLKPAHLVGDPTQDSLWRANT-----DRAFLR-- 88

QY 114 NSWESSRSGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRFOEIKENTKDKQVQYIY 173
Db 89 -----HGF-----SLSNLSLVITSGLYFYISQVFSGRGCPFRPTPTPLAHEVQ 135

QY 174 KYT-SYDPDPILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTN-EHLIDMD 231
Db 136 LPSPQYFPFHVPLLSAQKSVCPGQGPW-VRSVYQGAFLVLLTRGDQLSTHTDGSILL-LS 193

QY 232 HEASFFGAF 240
Db 194 PSSVFFGAF 202

RESULT 12
JQ1344
tumor necrosis factor alpha precursor - horse
N:Alternate names: cachectin; TNF alpha
C:Species: Equus caballus (domestic horse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JQ1344
R:Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
A:Reference number: JQ1344; MUID:92084125; PMID:1748301
A:Accession: JQ1344
A:Molecule type: DNA
A:Residues: 1-234 <SUX>

A:Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
C:Comment: This protein is an important proximal mediator of endotoxemia.
C:Genetics:
A:Gene: TNF-alpha
A:Introns: 62/3; 79/1; 95/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokines; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F:78-234/Product: tumor necrosis factor alpha #status predicted <TM>
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:146-178/Disulfide bonds: #status predicted

Query Match 9.8%; Score 126; DB 1; Length 234;
Best Local Similarity 22.5%; Pred. No. 0.0025;
Matches 45; Conservative 35; Mismatches 72; Indels 48; Gaps 9;

QY 62 ISTVQEKQ-----QNISPLVR-----ERGP-QRVAAHITGRGRSNTLSSPNSKNEKALG 110
Db 56 IGPQREEQLPNAFQSIINPLAQTLLRSSRTPSPDKPVAHVVA-----NPQAE 101

QY 111 RKINSWESSRSGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRFOEIKENTKDKQVQ 170
Db 102 QL--QWLSGRANALLANGVKLTQNLVPLDGLYISQVLFKQ-----GCPSTH 150

QY 171 YIYKYT-----SYDPDPILLMKSARNCSWCKDAEYG-----LYSIYQGGIFELKENDRIF 219
Db 151 VLLTHTISRLVSYPSKVNLLSAIKSPCHTESPEQAEAKPWPYPIYLGGVFQLEKGDLS 210

QY 220 VSVTNEHLLDMDHEAS-PFG 238
Db 211 ASINQPNYLDFAESGQVYFG 230

RESULT 13
QWJUN
tumor necrosis factor alpha precursor [validated] - human
N:Alternate names: cachectin; TNFA
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23;
R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
Nucleic Acids Res. 13, 6361-6373, 1985
A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro
A:Reference number: A93585; MUID:86016093; PMID:2995927
A:Accession: A93585
A:Molecule type: DNA
A:Residues: 1-233 <NED>
A:Cross-references: UNIPROT:P01375; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PJ
R:Iris, F.J.W.; Bouguetoret, L.; Prieur, S.; Caterina, D.; Frimas, G.; Perrot, V.; Jurka,
Nature Genet. 3, 137-145, 1993
A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A:Reference number: S36152; MUID:93272029; PMID:8499947
A:Accession: S36153
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-233 <IRI>
A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.,
Nature 312, 724-729, 1984
A:Title: Human tumour necrosis factor: precursor structure, expression and homology to l
A:Reference number: A93351; MUID:85086244; PMID:6392892
A:Accession: A93351
A:Molecule type: mRNA
A:Residues: 1-233 <PEN>
A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.;
Science 228, 149-154, 1985
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A:Reference number: A44189; MUID:85142190; PMID:3856324
A:Accession: A44189
A:Molecule type: mRNA

R; Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Masaki, N.; Nakamura, K.I.; Ar
Lymphokine Res. 7, 175-185, 1988
A; Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A; Reference number: A61478; MUID: 88301617; PMID: 2841543
A; Accession: A61478
A; Molecule type: protein
A; Residues: 56-79; 86-95, 'X', 97, 'X', 99; 119-151, 'XX', 154-162, 'X', 164, 'X', 166, 'X', 168, 'X', 1
R; Voigt, C.G.; Maurer-Poggy, I.; Adolfe, G.R.
FEBS Lett. 314, 85-88, 1992
A; Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylation
A; Reference number: S26951; MUID: 93083656; PMID: 1451807
A; Accession: S26951
A; Molecule type: protein
A; Residues: 35-59, 'N', 61-205 <VOI>
A; Note: 60-Thr was also found
R; Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.
Arch. Biochem. Biophys. 304, 144-153, 1993
A; Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO
A; Reference number: S34742; MUID: 93311995; PMID: 8323280
A; Contents: annotation
C; Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction,
while having no detrimental effect on normal cells. It can also act synergistically with
C; Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of differ
ical activities but are produced by different cell types and have different induction ki
C; Genetics:
A; Gene: GDB: LTA; LT; TNFB
A; Cross-references: GDB: 120442; OMIM: 153440
A; Map position: 6p21.3-6p21.3
A; Introns: 33/3; 69/1
A; Note: the first intron occurs before the initiator codon
C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage
F; 1-34/Domain: signal sequence #status predicted <SIG>
F; 35-205/Product: lymphotoxin #status predicted <AT>
F; 41/Binding site: carbohydrate (Thr) (covalent) #status experimental
F; 96/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 9.5%; Score 122; DB 1; Length 205;
Best Local Similarity 23.4%; Pred. No. 0.0046;
Matches 37; Conservative 29; Mismatches 72; Indels 20; Gaps 5;
QY 85 AAHITGRGNTLSGPNKNEKALGRKINSWESSRSHGSHFLNHLRNGELVTHEKGF 144
DB 64 AAHLIGDPSKQNSL-----LWANTDRAFLQGFSLNNSLIVPTSGIY 107
QY 145 YIYSQYFRQBEIKENTKNDKQMVQYIYKYTS-YDPILLMKRSARNSCWDAEYGLYS 203
DB 108 FVYSQVFSKAYSPRATSSPLLAHEVQLFSSQYPPHVELL-SSQKVVYPGLQEPWLHS 166
QY 204 IYOGGIFELKENDRIFVSVTN-EHLIDMDHEASFQAF 240
DB 167 MYHGAAPQLTQGDQLSTHTDGIPLHV-LSPSTVFFGAF 203

RESULT 15
QWNSN
tumor necrosis factor alpha precursor - mouse
N; Alternate names: cachectin; TNF alpha
C; Species: Mus musculus (house mouse)
C; Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 09-Jul-2004
C; Accession: A22908; S03791; A23127; A34251; I59058; A36696
R; Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
DNA 7, 193-201, 1988
A; Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis
A; Reference number: A22908; MUID: 88224564; PMID: 2836146
A; Accession: A22908
A; Molecule type: DNA
A; Residues: 1-235 <SHI>
R; Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A; Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl
A; Reference number: S03791; MUID: 87298639; PMID: 3040015

A; Accession: S03791
A; Molecule type: DNA
A; Residues: 1-235 <SHA>
A; Cross-references: GB: M38296; NID: G202086; PIDN: AAA0459.1; PID: G202087
A; Note: article in Russian with English abstract
R; Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A; Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor necr
A; Reference number: A93679; MUID: 88067722; PMID: 3684584
A; Accession: A27303
A; Molecule type: DNA
A; Residues: 1-235 <SEM>
R; Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A; Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosi
A; Reference number: A25164; MUID: 85298296; PMID: 3898078
A; Accession: A25164
A; Molecule type: mRNA
A; Residues: 1-235 <PEN>
A; Cross-references: GB: M11731; NID: G202084; PIDN: AAA0458.1; PID: G202085
R; Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, J.
Nucleic Acids Res. 13, 4417-4429, 1985
A; Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expres
A; Reference number: A23127; MUID: 85242112; PMID: 2989794
A; Accession: A23127
A; Molecule type: mRNA
A; Cross-references: GB: X02611; NID: G54844; PIDN: CAA26457.1; PID: G54845
R; Cseh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A; Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results
A; Reference number: A34251; MUID: 89380231; PMID: 2777790
A; Accession: A34251
A; Molecule type: protein
A; Residues: 70-87 <CSE>
R; Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A; Title: Identification of a common nucleotide sequence in the 3'-untranslated region of
A; Reference number: I59058; MUID: 86149365; PMID: 2419912
A; Accession: I59058
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-230, 'R', 232-235 <RES>
A; Cross-references: GB: M13049; NID: G202082; PIDN: AAA0457.1; PID: G202083
R; Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A; Title: Characterization of high molecular weight glycosylated forms of murine tumor necr
A; Reference number: A36696; MUID: 91097531; PMID: 2268312
A; Accession: A36696
A; Molecule type: protein
A; Residues: 80-85, 'X', 87-99 <SHE>
C; Genetics:
A; Introns: 62/3; 81/1; 97/1
A; Note: the first intron occurs in the 5'-untranslated region
C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F; 80-235/Product: tumor necrosis factor #status experimental <MAT>
F; 20/Binding site: myristate (Lys) (covalent) #status predicted
F; 84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 148-179/Disulfide bonds: #status predicted

Query Match 9.4%; Score 121; DB 1; Length 235;
Best Local Similarity 23.1%; Pred. No. 0.0066;
Matches 43; Conservative 34; Mismatches 79; Indels 30; Gaps 8;
QY 67 EKOQNTSLVRERGQORVAHITGTRGNTLSGP-----NSKNEKALGRKINSWESSR 120
DB 62 EKFPNGPLI-----SSMAQTTLTRSSSQNSDKPVAHVAVNHQVBEQL-----EWLSQR 111
QY 121 SGHSFLSNLHNLNGELVTHEKGFYIYSQYTFPFQBEIKENTKNDKQMVQYIYKYT-SYP 179
A; Reference number: S03791; MUID: 87298639; PMID: 3040015

Db 112 ANALLANGMDLKNQJVPADGLYLVSQVLFKGQ-----GCPDYVLLTHTVSRFAISYQ 166
Qy 180 DPILLMKSARNSCWSKDAEYG-----LYSIYGGIFELKENDRIFVSVTNEHLIDMDHE 233
Db 167 EKVNLLSAVKSPC-PKOTPEGAELKEWYEPYILGGVFQLEKGDQLSAEVLNPKYLDFAES 225
Qy 234 AS-FFG 238
Db 226 GOVYFG 231

Search completed: June 22, 2005, 06:03:13
Job time : 24.187 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 100.168 Seconds
(without alignments)
1242.266 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYKSGTACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1287	100.0	281	1	TN10_HUMAN
2	879	68.3	287	2	Q8K3G0
3	863	67.1	291	1	TN10_MOUSE
4	703.5	54.7	304	2	Q7T1F2
5	515.5	40.1	299	2	Q6DHG9
6	307.5	23.9	317	2	Q7ZVX9
7	305.5	23.7	214	2	Q9DDZ5
8	305	23.7	287	2	Q90WT9
9	291	22.6	63	2	Q6JSD9
10	250.5	19.5	318	1	TN11_RAT
11	238.5	18.5	316	1	TN11_MOUSE
12	235.5	18.3	317	1	TN11_HUMAN
13	189.5	14.7	279	1	TN10_MOUSE
14	185.5	14.4	280	1	TN10_MOUSE
15	184.5	14.3	279	2	Q7TMV9
16	183.5	14.3	280	1	TN10_MOUSE
17	183.5	14.3	280	1	TN10_MOUSE
18	183.5	14.3	280	1	TN10_MOUSE
19	182.5	14.2	281	1	TN10_MOUSE
20	182	14.1	282	1	TN10_MOUSE
21	180	14.0	252	2	Q8K3Y8
22	177.5	13.8	278	1	TN10_MOUSE
23	176.5	13.7	280	2	Q861W5
24	175.5	13.6	169	2	Q9WV90
25	175	13.6	252	2	Q80VZ0
26	173	13.4	252	2	Q8K3Y7
27	171	13.3	272	1	TN10_MOUSE
28	166	12.9	251	2	Q8NFE9
29	163.5	12.7	131	2	Q6J306
30	160	12.4	174	1	TN10_MOUSE
31	159.5	12.4	240	1	TN10_MOUSE

32	157	12.2	154	2	Q8MJ19
33	152.5	11.8	229	1	TN14_MOUSE
34	152	11.8	261	1	TN10_BOVIN
35	151.5	11.8	227	2	Q7T2Q3
36	144.5	11.2	216	2	O70332
37	143	11.1	241	2	Q6U817
38	141	11.0	231	2	Q8AW02
39	140	10.9	261	1	TN10_MOUSE
40	140	10.9	261	1	TN10_MOUSE
41	137.5	10.7	232	2	Q80XA4
42	137.5	10.7	234	2	Q6T9C7
43	137.5	10.7	260	1	TN10_MOUSE
44	137	10.6	261	1	TN10_MOUSE
45	137	10.6	261	1	TN10_MOUSE

ALIGNMENTS

RESULT 1			
TN10_HUMAN	STANDARD;	PRT;	281 AA.
AC	P50591;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related		
DE	apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).		
GN	Name=TNFSF10; Synonyms=APO2L, TRAIL;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RX	MEDLINE=9611195; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;		
RA	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,		
RA	Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,		
RA	Goodwin R.G.;		
RT	"Identification and characterization of a new member of the TNF family		
RT	that induces apoptosis.";		
RL	Immunity 3:673-682(1995).		
RN	[2]		
RX	MEDLINE=96278649; PubMed=8663110; DOI=10.1074/jbc.271.22.12687;		
RA	Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,		
RA	Ashkenazi A.;		
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor		
RT	necrosis factor cytokine family.";		
RL	J. Biol. Chem. 271:12687-12690(1996).		
RN	[3]		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,		
RA	Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		

RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
RX MEDLINE=20017054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80207-5;
RA Hymowitz S.G., Christinger H.W., Fuh G., Uitsch M., O'Connell M.,
RA Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
RT complex with death receptor 5.";
RL Mol. Cell 4:563-571(1999).
RN [5]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
RX PubMed=10542098; DOI=10.1038/14935;
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RA Jones E.Y., Screaton G.R.;
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT specificity in apoptotic initiation.";
RL Nat. Struct. Biol. 6:1048-1053(1999).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
RX MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;
RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
RA Sung Y.C., Oh B.-H.;
RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with
RT selective antitumor activity.";
RL Immunity 11:253-261(1999).
CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1.
CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC may be modulated by binding to the decoy receptors
CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC induce apoptosis.
CC -1- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
CC trimer.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung
CC and prostate.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC EMBL; U37518; AAC50332.1; -;
CC EMBL; U57059; AAB01233.1; -;
CC EMBL; BC032722; AAH32722.1; -;
CC PDB; 1D0G; X-ray; A/B/D=114-281.
CC PDB; 1D2Q; X-ray; A=114-281.
CC PDB; 1D4V; X-ray; B=119-281.
CC PDB; 1D66; X-ray; A=91-281.
CC PDB; 1D03; X-ray; D/E/F/G/K/L=114-281.
CC Genew; HGNC:11925; TNFSF10.
CC H-InvDB; HIX0003863; -;
CC MIM; 603598; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005625; C:soluble fraction; TAS.
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0006917; P:induction of apoptosis; TAS.
CC GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB; IEP.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS00049; TNF 2; 1.
KW 3D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor;
KW Transmembrane; Zinc.
FT DOMAIN 1 17 Cytoplasmic (Potential).
FT TRANSMEM 18 38 Signal-anchor for type II membrane
FT DOMAIN 39 281 protein (Potential).
FT METAL 230 230 Extracellular (Potential).
FT STRAND 123 127 Zinc.
FT STRAND 149 150
FT STRAND 163 165
FT STRAND 167 170
FT TURN 171 172
FT STRAND 173 176
FT STRAND 180 193
FT TURN 198 199
FT STRAND 205 213
FT STRAND 220 228
FT TURN 233 234
FT STRAND 237 250
FT TURN 252 253
FT STRAND 255 260
FT STRAND 263 265
FT HELIX 266 267
FT STRAND 270 272
FT TURN 274 279
SQ SEQUENCE 281 AA; 32509 MW; DDAAF78DAAB2F6D CRC64;

Query Match 100.0%; Score 1287; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELQMDDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVQWQLRQLVRKMLTSEE 60
DB 39 TNELQMDDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVQWQLRQLVRKMLTSEE 98
QY 61 TISTVQEKQNTISPLVRERGQORVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNTISPLVRERGQORVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHLRNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQMYIYKYTSYDP 180
DB 159 SGHSFLSNLHLRNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQMYIYKYTSYDP 218
QY 181 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281

RESULT 2
Q8K3G0 PRELIMINARY; PRT; 287 AA.
ID AC Q8K3G0;
DC DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
OS TNF-related apoptosis inducing ligand.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA;
RA Mueller A.M., Giegerich G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY115578; AAM49797.1; -;
DR HSSP; P50591; 1D2Q.
DR GO; GO:0016020; C:membrane; IEA.

DR GO: GO:0005164; P: tumor necrosis factor receptor binding; IEA.
 DR GO: GO:0006955; P: immune response; IEA.
 DR InterPro: IPR006032; TNF family.
 DR InterPro: IPR008983; TNF like.
 DR Pfam: PF00229; TNF; 1.
 DR ProDom: PD002012; TNF subf; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; UNKNOWN_1.
 DR PROSITE: PS0049; TNF_2; 1.
 DR SEQUENCE 287 AA; 33979 MW; CA4F5B5D7C933PEC CRC64;
 Query Match 68.3%; Score 879; DB 2; Length 287;
 Best Local Similarity 69.7%; Pred. No. 5.2e-64;
 Matches 170; Conservative 25; Mismatches 43; Indels 6; Gaps 2;
 QY 2 NELKQMDKYSGKGIACFLKEDSDSYDPNDDESMNSPCWQVQWQLRQLVRKMLRTSEET 61
 DB 44 NEVKQLQDNYSKIGLACFSKDEGDFWSDTDEGLNRPCLQVQRQLYLTIEVLTFTFEK 103
 QY 62 ISTVQEKQONISPLVREGRQPVAAHITGTRGRSNTLSSPNSKVEKALGRKINSWESSR 121
 DB 104 ISTVPEKQLSTPLPRGRPRQPVAAHITGTRSNLALIPISKDGLTQKQIETWESSR 163
 QY 122 GHSFLNLHLNGLVHEKGYIYSQTYFRQEE--EIKENTKND-----KQWVQYIYKY 175
 DB 164 GHSFLNLHLNGLVHEKGYIYSQTYFRQEE--EIKENTKND-----KQWVQYIYKY 223
 QY 176 TSYDPDILLMKMSARNCSWCKDAEYGLYSIQGIFELKENDRIFVSVTNEHLMDLDEAS 235
 DB 224 TSYDPDILLMKMSARNCSWCKDAEYGLYSIQGIFELKENDRIFVSVTNEHLMDLDEAS 283
 QY 236 PFGA 239
 DB 284 PFGA 287
 RESULT 3
 TN10_MOUSE STANDARD; PRT; 291 AA.
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 apoptosis inducing ligand) (TRAIL protein).
 GN Name=TNFsf10; Synonyms=Trail;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;
 RA WILEY S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C.A.,
 RA Goodwin R.G.;
 RT Identification and characterization of a new member of the TNF family
 that induces apoptosis.
 RL Immunity 3:673-682(1995).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1.
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Widespread.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 or send an email to license@ebi-sib.ch).
 CC -----
 DR EMBL: U37522; AAC52345.1; --
 DR HSSP: P50591; 1D2Q.
 DR MGD: MGI:107414; Tnf9f10.
 DR InterPro: IPR006032; TNF family.
 DR InterPro: IPR008983; TNF like.
 DR Pfam: PF00229; TNF; 1.
 DR ProDom: PD002012; TNF subf; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS0049; TNF_2; 1.
 KW Apoptosis; Cytokine; Signal-anchor; Cytoplasmic (Potential).
 FT DOMAIN 1 17
 FT TRANSMEM 18 38
 FT DOMAIN 39 291
 FT CARBOHYD 52 52
 FT CARBOHYD 52 52
 SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;
 Query Match 67.1%; Score 863; DB 1; Length 291;
 Best Local Similarity 66.1%; Pred. No. 1.1e-62;
 Matches 164; Conservative 32; Mismatches 46; Indels 6; Gaps 1;
 QY 1 TNELKQMDKYSGKGIACFLKEDSDSYDPNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 60
 DB 43 TNELKQMDKYSGKGIACFLKEDSDSYDPNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 102
 QY 61 TISTVQEKQONISPLVREGRQPVAAHITGTRGRSNTLSSPNSKVEKALGRKINSWESSR 120
 DB 103 TISTVPEKQLSTPLPRGRPRQPVAAHITGTRSNLALIPISKDGLTQKQIETWESSR 162
 QY 121 GHSFLNLHLNGLVHEKGYIYSQTYFRQEE-----IKENTKNDKQWVQYIYK 174
 DB 163 GHSFLNLHLNGLVHEKGYIYSQTYFRQEE-----IKENTKNDKQWVQYIYK 222
 QY 175 YTSYDPDILLMKMSARNCSWCKDAEYGLYSIQGIFELKENDRIFVSVTNEHLMDLDEA 234
 DB 223 YTSYDPDILLMKMSARNCSWCKDAEYGLYSIQGIFELKENDRIFVSVTNEHLMDLDEA 282
 QY 235 SFFGAFLV 242
 DB 283 SFFGAFLI 290
 RESULT 4
 Q7TIF2 PRELIMINARY; PRT; 304 AA.
 ID Q7TIF2;
 AC Q7TIF2;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Tumor necrosis factor related apoptosis inducing ligand.
 GN Name=TRAIL;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Sayed A.A., Horiuchi H., Furusawa S., Matsuda H.;
 RT "Molecular Cloning and Characterization of Chicken Tumor Necrosis
 RT Factor (TNF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis
 RT Inducing Ligand (TRAIL).";
 RL J. Vet. Med. Sci. 66:643-650(2004).
 DR EMBL: AB114678; BAC79267.1; --


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QY 65 VOEKQ---NISP-LVRGPPQVAHI-----TGTRGRSNTLSPNSKNEKALGR 111
DB 103 VNEAQKSYENISGGVATKTLGKPSAHLFRPQNPAGDSSRRFGNLS-----QSCRH 155
QY 112 KINSWESSGHSFLNLHRLNCELVIHEKGFYIYSQYFRQBEIKENTKNDKQVQY 171
DB 156 AITRWEDS-TIISHLQNIITVRDGLRVNQAGKYVYSQIYFRYSDRGAGARVSPQLVQC 214
QY 172 IYKTSYPPDILLMKARSNSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMD 231
DB 215 INWKTSYQIPILLKGVGKTCWAPAEYGLHLYQGLFELKAGDELFSVSSLAIDYSD 274
QY 232 HEASFFGAF 240
DB 275 AASYFGAF 283

RESULT 9
Q6JSD9 PRELIMINARY; PRT; 63 AA.
AC O6JSD9;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Chemokine tumor necrosis factor ligand superfamily member 10
DE (Fragment).
GN Name=TNFSF10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RA Poivi A., Ruosaari S., Vendelin J., West A., Saarikko I.,
RA Reinikainen A., Hollmen J., Laitinen T., Mannila H., Lahesmaa R.,
RA Kere J.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV312579; AAR16184.1; -.
FT NON_TER 1 1
SQ SEQUENCE 63 AA; 7638 MW; 8F0C7936DA5AA6E6 CRC64;

Query Match 22.6%; Score 291; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGIACFLKEDDSYNDPNDESMNSPCWQVKWQLRQLVRK 52
DB 1 TNELKQMDKYSGIACFLKEDDSYNDPNDESMNSPCWQVKWQLRQLVRK 52

RESULT 10
TN11 RAT STANDARD; PRT; 318 AA.
AC Q9SE2; Q91219;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE differentiation factor) (ODF).
GN Name=TNfrsf11; Synonyms=Oppl, Rankl, Trance;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibial bone;
RX MEDLINE=20540945; PubMed=11092398;
RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,

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RA Zheng M.H.;
RT "Cloning, sequence and functional characterization of the rat
RT homologue of receptor activator of NF-kB ligand.";
RL J. Bone Miner. Res. 15:2178-2186(2000).
RN [2]
RP SEQUENCE OF 266-318 FROM N.A.
RC STRAIN=Fischer 344;
RX MEDLINE=21662371; PubMed=11804028;
RA Odgren P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savas A.,
RA Safadi P.P., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
RA Marks S.C. Jr.;
RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";
RL Int. J. Dev. Biol. 45:853-859(2001).
CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC Augments the ability of dendritic cells to stimulate naive T-cell
CC proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcemia of malignancy.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: type II membrane protein and secreted (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
DR EMBL; AF187319; AAG17031.1; -.
DR EMBL; AF425669; AAL23963.1; -.
DR HSSP; OJ5235; 1JTZ.
DR GSD; 620784; tnfsf11.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Differentiation; Glycoprotein; Receptor; Signal-anchor;
KW Transmembrane.
FT CHAIN 1 318 Tumor necrosis factor ligand superfamily
FT member 11, membrane form.
FT CHAIN 141 318 Tumor necrosis factor ligand superfamily
FT member 11, soluble form.
FT DOMAIN 1 47 Cytoplasmic (Potential).
FT TRANSMEM 48 68 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 69 318 Extracellular (Potential).
FT SITE 140 141 Cleavage (By similarity).
FT CARBOHYD 199 199 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 264 264 N-linked (GlcNAc...) (Potential).
FT CONFLICT 317 317 I -> M (in Ref. 2).
SQ SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD098F CRC64;

Query Match 19.5%; Score 250.5; DB 1; Length 318;
Best Local Similarity 28.5%; Pred. No. 2.4e-12;
Matches 75; Conservative 46; Mismatches 87; Indels 55; Gaps 10;

QY 9 DKYSKGIACF-----LKED----DSYNDPNDESMNSPCWQVKWQLRQLVRKLTSE 59
DB 78 NRISDSTCFYRLRLRENTGLQDSTLESDTEALPDCRRWKQAFQ----- 125

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QY 60 ETISTVQKQNTSPLVRGPOR---VAAHITGT-----RGRS-----NTLSS 100
 Db 126 ---GAVQRELQHV-----GPRFSGVPANMEGSLDVARGKPEAQPPFAHLTINADI 176
 QY 101 PNSNKKALGRKINSMESSRSHSFLSNLRLNGELVIHEKGYFYIYSQTYFRPQEEIKE 160
 Db 177 PSQSHKVSU-----SSWYHDR-GWAKISNMTLSNGLRVNQDGFYLYANICFRHETSQS 231
 QY 161 NTKNDQKQWQYIYKT-SYDDPILLMKSARNSCWDKDAEGLVSIYGGIFELKENDRIF 219
 Db 232 VPADYLQLMVYVVKTSIKIPSSHNLMKGGSTKQNSGNSBFHYSINVGGFFKLAGEBIS 291
 QY 220 VSVTNEHLIDMDHEASFFGAFLV 242
 Db 292 VQVSNPSLLDPDQATYFGAKV 314

RESULT 11

TN11 MOUSE STANDARD; PRT; 316 AA.

AC Q35235; Q35306; Q9JUK8; Q9JUK9; Q9RIY0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
 DE (OCIF).
 GN Names=Tnfsl1; Synonyms=OPGL, RANKL, Trance;
 OS Mus musculus (Mouse)
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hybridoma;
 RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
 RA Kalachikov S., Cayani E., Bartlett P.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells.";
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thymic lymphoma;
 RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/365593;
 RA Anderson D.W., Maraskovsky E., Billingsley W.D., Dougall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
 RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow;
 RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
 RA Boyle W.J.;
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
 RT differentiation and activation.";
 RL Cell 93:165-176(1998).
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow stroma;
 RX MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
 RA Mochizuki S.-I., Tomoyasu A., Iano K., Goto K., Murakami A., Tsuda E.,

RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
 RT "Osteoclast differentiation factor is a ligand for
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
 RT to TRANCE/RANKL.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
 RN [5]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=129;
 RX MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
 RA Ueda M., Higashio K.;
 RT "Cloning and characterization of the gene encoding mouse osteoclast
 RT differentiation factor.";
 RL Gene 230:121-127(1999).
 RN [6]
 RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
 RT "Determination of three isoforms of the receptor activator of nuclear
 RT factor-kappaB ligand and their differential expression in bone and
 RT thymus.";
 RL Endocrinology 142:1419-1426(2001).
 RN [7]
 RN SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
 RX MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
 RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
 RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
 RT "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
 RT converting enzyme-like protease in shedding of TRANCE, a TNF family
 RT member involved in osteoclastogenesis and dendritic cell survival.";
 RL J. Biol. Chem. 274:13613-13618(1999).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
 RX MEDLINE=21464816; PubMed=11581298;
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
 RT of receptor-ligand specificity.";
 RL J. Clin. Invest. 108:971-979(2001).
 RN [9]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
 RX MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;
 RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at
 RT 2.2-A resolution.";
 RL J. Biol. Chem. 277:6631-6636(2002).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O35235-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O35235-2; Sequence=VSP_006449;
 CC Name=3;
 CC IsoId=O35235-3; Sequence=VSP_006448;
 CC -1- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
 CC but not in nonlymphoid tissues and is abundantly expressed in T
 CC cells but not in B cells. A high level expression is also seen in
 CC the trabecular bone and lung.
 CC -1- PTM: N-glycosylated.
 CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing. The cleavage may be catalyzed by
 CC ADAM17. A further shorter soluble form was observed.
 CC -1- DISEASE: Deficiency in tnfrsf11 results in failure to form lobulo-

RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
 RA Wong B R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Lee S.Y.,
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "TRANSC is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells.";
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [5];
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=tongue;
 RA MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
 RA Nagai M., Kyakumoto S., Sato N.;
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA
 RT encoding a secreted form of ODF/TRANSC that induces osteoclast
 RT formation.";
 RL Biochem. Biophys. Res. Commun. 269:532-536(2000).
 CC -I- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -I- SUBUNIT: Homotrimer (By similarity).
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
 CC Secreted (isoform 2). A soluble form of isoform 1 arises by
 CC proteolytic processing (By similarity).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O14788-1; Sequence=Displayed;
 CC Name=2; Synonyms=SODF;
 CC IsoId=O14788-2; Sequence=VSP_006447;
 CC Name=3;
 CC IsoId=O14788-3; Sequence=VSP_006446;
 CC -I- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
 CC spleen, peripheral blood leukocytes, bone marrow, heart, placenta,
 CC skeletal muscle, stomach and thyroid.
 CC -I- INDUCTION: Up-regulated by T cell receptor stimulation.
 CC -I- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing (By similarity). The cleavage may be
 CC catalyzed by ADAM17.
 CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF019047; AB86811.1; -;
 CC EMBL; AF053712; AAC39731.1; -;
 CC EMBL; AB064269; BAB79694.1; -;
 CC EMBL; AB061227; BAB71768.1; -;
 CC EMBL; AB064270; BAB79695.1; -;
 CC EMBL; AF013171; AAC51762.1; -;
 CC EMBL; AB037599; BAA90488.1; -;
 CC HSSP; O35235; IJTZ.
 CC Genew; HGNC:11926; TNFSF11.
 CC MIM; 602642; -;
 CC GO; GO:0005576; C:extracellular; NAS.
 CC GO; GO:0005887; C:integral to plasma membrane; NAS.
 CC GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
 CC GO; GO:0006955; P:immune response; NAS.
 CC GO; GO:0030316; P:osteoclast differentiation; NAS.
 CC InterPro; IPR006052; TNF family.
 CC InterPro; IPR008983; TNF-like.
 CC InterPro; IPR003636; TNF_subf.
 CC Pfam; PF00229; TNF; 1.
 CC ProDom; PD002012; TNF_subf; 1.

DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; FALSE_NEG.
 DR PROSITE; PS00049; TNF_2; 1.
 KW Alternative splicing; Cytokine; Differentiation; Glycoprotein;
 KW Receptor; Signal-anchor; Transmembrane.
 FT CHAIN 1 317
 FT member 11, membrane form.
 FT CHAIN 140 317
 FT member 11, membrane form.
 FT Tumor necrosis factor ligand superfamily
 FT member 11, soluble form (By similarity).
 FT CYTOPLASMIC (Potential).
 FT Signal-anchor for type II membrane
 FT protein (Potential).
 FT Extracellular (Potential).
 FT Cleavage (By similarity).
 FT SITE 139 171
 FT CARBOHYD 171 171
 FT CARBOHYD 198 198
 FT VARSPLIC 1 47
 FT Missing (in isoform 3).
 FT FTId=VSP_006446.
 FT VARSPLIC 1 73
 FT Missing (in isoform 2).
 FT FTId=VSP_006447.
 FT CONFLICT 194 194
 FT A -> G (in Ref. 4).
 SQ SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;
 Query Match 18.3%; Score 235.5; DB 1; Length 317;
 Best Local Similarity 25.3%; Pred. No. 4.1e-11;
 Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;
 QY 9 DKYSGGIACF-----LKED----DSYMDPNDSESMNSPCWQVKW-----QLRQLVR 51
 DB 77 NRISGDGTHCIYRLLEHENAFOQTTLSESDTKLPDSCRRKIQAFQAGVQKELHIVG 136
 QY 52 KMLRTSEETI-----STVOEKQONISPLVRGPRQVAHITGTRGNTLSPNSKNE 106
 DB 137 SQHRAEKAMVDGSMLDLAKRSKLEAQP-----AHLT-----INATDIPSGSHK 181
 QY 107 KALGRKINSEWSRSCHSPSLNHLNGLVTHEKGFYIYSQTYFRFOEEIKENTKNDK 166
 DB 182 VSL-----SSWYHNR-GWAKISNMTFSGKLIYNQDGFYLYANICFRHHETSGDLATEYL 236
 QY 167 QMVOYIKYT-SYDPDILLKMGARNCSKDAEYGLYSYVQGGIFELKENDRIFVSVTNE 225
 DB 237 QLMVYVTKTSIKIPSSHTLMKGGSTKYNSGNSEFPFYSINVGFFKLRSGEESIEVSNP 296
 QY 226 HLIDMDHEASFFGAFIV 242
 DB 297 SLLDPDQDATYFGAFKV 313
 RESULT 13
 TNF6_MOUSE STANDARD; PRT; 279 AA.
 ID P41047; O61217; O9R1F2;
 AC P41047; O61217; O9R1F2;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
 DE ligand).
 GN Name=Tnf6; Synonyms=APTLG1, FasL, gld;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX MEDLINE=94185175; PubMed=7511063; DOI=10.1016/0092-8674(94)90375-1;
 RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
 RA Suda T., Nagata S.;
 RT "Generalized lymphoproliferative disease in mice, caused by a point
 RT mutation in the Fas ligand";
 RL Cell 76:969-976(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
 RC STRAIN=C57BL/6;

RX MEDLINE=95388076; PubMed=7544870; DOI=10.1016/0161-5890(95)00016-8;
RA Peitsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
of the TNF family."; Mol. Immunol. 32:761-772(1995).
RL [3]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RP MEDLINE=95196085; PubMed=7889405; DOI=10.1016/1074-7613(94)90106-6;
RX Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF
family gene cluster."; Immunol. 113:131-136(1994).
RL [4]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RP STRAIN=BALB/c;
RC Fenner M.H., Shioda T., Isselbacher K.J.;
RA "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in two
amino acids."; Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RL [5]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RP STRAIN=C3H; TISSUE=Spleen;
RX MEDLINE=20021694; PubMed=10552956;
RA Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
RA Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
RT "Cloning and expression of a short Fas ligand: a new alternatively
spliced product of the mouse Fas ligand gene."; Blood 94:3456-3467(1999).
RL [6]
RN CHARACTERIZATION OF VARIANT GLD.
RP MEDLINE=96091792; PubMed=7495745;
RX Hahne M., Peitsch M.C., Irmiler M., Schroeter M., Lowin B.,
RA Rouseau M., Bron C., Renno T., French L., Tschopp J.;
RT "Characterization of the non-functional Fas ligand of gld mice."; Int. Immunol. 7:1381-1386(1995).
RL [7]
RN STRAIN=ALA-184 and GLY-218.
RP STRAIN=BALB/c, C3H, C57BL/6, DBA/1, DBA/2, MRL, NOD, NZB, NZW, and
RC SJL;
RX MEDLINE=97268671; PubMed=9108079; DOI=10.1073/pnas.94.8.3914;
RA Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,
RA Yagita H.;
RT "Polymorphism of murine Fas ligand that affects the biological
activity."; Acad. Sci. U.S.A. 94:3914-3919(1997).
RL [8]
RN FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
transduces the apoptotic signal into cells. May be involved in
cytotoxic T cell mediated apoptosis and in T cell development.
TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
peripheral tolerance, in the antigen-stimulated suicide of mature
T cells, or both. Binding to the decoy receptor TNFRSF6B/Dcr3
modulates its effects (By similarity).
CC -1- SUBUNIT: Homotrimer (Probable).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
Secreted (isoforms FASL and FASLS).
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=FasL;
IsoId=P41047-1; Sequence=Displayed;
Name=FasLS;
IsoId=P41047-2; Sequence=VSP_006445;
CC -1- PTM: The soluble form derives from the membrane form by
proteolytic processing (By similarity).
CC -1- DISEASE: A deficiency in this protein is the cause of generalized
lymphoproliferation disease phenotype (gld). Gld mice present
lymphadenopathy and autoantibody production. The phenotype is
recessively inherited.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.

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or send an email to license@isb-sib.ch).

DR EMBL; U06948; AAA17800.1; -
DR EMBL; U10984; AAA19778.1; -
DR EMBL; S76752; AAB33780.1; -
DR EMBL; U58995; AAB02915.1; -
DR EMBL; AF119335; AAD52106.1; -
DR PIR; A53062; A53062.
DR HSP; P50591; I066.
DR MGD; MGI:99255; tnfsf6.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00449; TNF_2; 1.
KW Alternative splicing; Apoptosis; Cytokine; Disease mutation;
Glycoprotein; Polymorphism; Signal-anchor; Transmembrane.
FT CHAIN 1 279
Tumor necrosis factor ligand superfamily
member 6, membrane form.
FT CHAIN 128 279
Tumor necrosis factor ligand superfamily
member 6, soluble form (By similarity).
FT DOMAIN 1 78
Cytoplasmic (Potential).
FT TRANSMEM 79 100
Signal-anchor for type II membrane
protein (Potential).
FT DOMAIN 101 279
Extracellular (Potential).
FT DOMAIN 4 59
Pro-rich.
FT DOMAIN 45 51
Poly-Pro.
FT SITE 127 128
Cleavage (By similarity).
FT DISULFID 200 231
Potential.
FT CARBOHYD 117 117
N-linked (GlcNAc..) (Potential).
FT CARBOHYD 182 182
N-linked (GlcNAc..) (Potential).
FT CARBOHYD 248 248
N-linked (GlcNAc..) (Potential).
FT CARBOHYD 258 258
Missing (in isoform FASLS).
FT VARSPLIC 1 210
/FTID=VSP_006445.
FT VARIANT 184 184
T -> A (in strain BALB/c, strain DBA/1
and strain DBA/2; enhances cytotoxicity).
FT VARIANT 218 218
E -> G (in strain BALB/c, strain DBA/1
and strain DBA/2; enhances cytotoxicity).
FT VARIANT 273 273
F -> L (in gld; abolishes binding of FASL
to its receptor).
SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;
Query Match 14.7%; Score 189.5; DB 1; Length 279;
Best Local Similarity 25.8%; Pred. No. 2.1e-07;
Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;
QY 45 QLRLVRKMLRTSETISTVQEKQONISPLVRERGPQVAAHITGRSNTLSPNSK 104
Db 111 ELREFTNQSL-----KVSSFEKQIANPTPEKPRSV-AHLTG-----NPHSR 154
QY 105 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVLTHKGYPYIYQSYQYFPRFQBEIKENTKN 164
Db 155 SIPL-----EWEDT-VGTALISGVKYGKGLVINETGLYFVYKVFYRQ-----SCN 201
QY 165 DKQMVOYIY-KYTSYDPDILLMKSR-NSCWKSDAEVGLSYIQGGIFELKENDRIFVSV 222
Db 202 NQPLNKHVYMRNSKYPEDLVLMEEKLNLYCTT--GQIWAHSSYLGAVFNLTSDHLYVNI 259
QY 223 TNEHLIDMDHEASFFGCA 240
Db 260 SQLSLINFEESKTFGLY 277

RESULT 14

ID	TNF6_CERTO	STANDARD;	PRT;	280 AA.
AC	Q9BDN1;			
DT	28-FEB-2003	(Rel. 41, Created)		
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	03-JUL-2004	(Rel. 44, Last annotation update)		
DE	Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)			
DE	(CD95L protein)			
GN	NAME=TNFSF6; Synonym=CD95L, FASL;			
OS	Cercobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Cercopithecinae; Cercopithecidae;			
OC	NCBI_TaxID=9531;			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Lymphocytes;			
RC	MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;			
RC	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,			
RC	Weiss W.R., Ansari A.A.;			
RT	"Cloning, sequencing, and homology analysis of nonhuman primate			
RT	Fas/Pas-ligand and co-stimulatory molecules.";			
RL	Immunogenetics 53:315-328(2001).			
CC	-!- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that			
CC	transduces the apoptotic signal into cells. May be involved in			
CC	cytotoxic T cell mediated apoptosis and in T cell development.			
CC	TNFSF6/FAS-mediated apoptosis may have a role in the induction of			
CC	peripheral tolerance, in the antigen-stimulated suicide of mature			
CC	T cells, or both. Binding to the decoy receptor TNFRSF6B/CDK3			
CC	modulates its effects (By similarity).			
CC	-!- SUBUNIT: Homotrimer (Probable).			
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By			
CC	similarity).			
CC	-!- PTM: The soluble form derives from the membrane form by			
CC	proteolytic processing (By similarity).			
CC	-!- SIMILARITY: Belongs to the tumor necrosis factor family.			
CC				
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CC	or send an email to license@sib-sib.ch).			
CC				
DR	EMBL; AF344847; AK37606.1; --			
DR	HSSP; P50591; ID20.			
DR	InterPro; IPR008064; Fas ligand.			
DR	InterPro; IPR006053; TNF abc.			
DR	InterPro; IPR006052; TNF family.			
DR	InterPro; IPR008983; TNF-like.			
DR	InterPro; IPR003636; TNF_subf.			
DR	Pfam; PF00229; TNF; 1.			
DR	PRINTS; PR01681; FASLIGAND.			
DR	PRINTS; PR01234; TNECROSISFCT.			
DR	ProDom; PD002012; TNF_subf; 1.			
DR	SMART; SM00207; TNF; 1.			
DR	PROSITE; PS00351; TNF_1; 1.			
DR	PROSITE; PS0049; TNF_2; 1.			
KW	Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.			
FT	FT	Tumor necrosis factor ligand superfamily		
FT	FT	member 6, membrane form.		
FT	FT	Tumor necrosis factor ligand superfamily		
FT	FT	member 6, soluble form (By similarity).		
FT	FT	Cytoplasmic (Potential).		
FT	FT	Signal-anchor for type II membrane		
FT	FT	protein (Potential).		
FT	FT	Extracellular (Potential).		
FT	FT	Pro-rich.		
FT	FT	Poly-Pro.		
FT	FT	Cleavage (By similarity).		
FT	FT	Potential.		

FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 249 249 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 259 259 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 280 AA; 31407 MW; 729EA6067B7D398 CRC64;

Query Match 14.4%; Score 185.5; DB 1; Length 280;

Best Local Similarity 27.4%; Pred. No. 4.4e-07;

Matches 55; Conservative 42; Mismatches 77; Indels 27; Gaps 8

QY	44	WOLRVLKMI-LR--TSSEITSTVOEKQINISPLVRGQQRVAAHITGRGRSNTLSS	100
DB <td>101 <td>FQFLHQLKELAEALRESTSQKHTASSLEKQIGHPSPPPEKKQKVAHLTG-----K <td>151</td> </td></td>	101 <td>FQFLHQLKELAEALRESTSQKHTASSLEKQIGHPSPPPEKKQKVAHLTG-----K <td>151</td> </td>	FQFLHQLKELAEALRESTSQKHTASSLEKQIGHPSPPPEKKQKVAHLTG-----K <td>151</td>	151
QY <td>101 <td>PNSKNEKALGRKINSWSSRSRSHSFLNLHLRNGELVIEHKGFIYYSQTYFRQESEIKE <td>160</td> </td></td>	101 <td>PNSKNEKALGRKINSWSSRSRSHSFLNLHLRNGELVIEHKGFIYYSQTYFRQESEIKE <td>160</td> </td>	PNSKNEKALGRKINSWSSRSRSHSFLNLHLRNGELVIEHKGFIYYSQTYFRQESEIKE <td>160</td>	160
DB <td>152 <td>PNSRSMP-----EWEDT-YGIVLLSGVKYKKGGLVNETGLTYFVYSKVYFRGQ----- <td>199</td> </td></td>	152 <td>PNSRSMP-----EWEDT-YGIVLLSGVKYKKGGLVNETGLTYFVYSKVYFRGQ----- <td>199</td> </td>	PNSRSMP-----EWEDT-YGIVLLSGVKYKKGGLVNETGLTYFVYSKVYFRGQ----- <td>199</td>	199
QY <td>161 <td>NTNDKQVMQYIY-KYTSYPPDILLKMSARNSCWSKDAEGLYSIQGIFELKENDRIF <td>219</td> </td></td>	161 <td>NTNDKQVMQYIY-KYTSYPPDILLKMSARNSCWSKDAEGLYSIQGIFELKENDRIF <td>219</td> </td>	NTNDKQVMQYIY-KYTSYPPDILLKMSARNSCWSKDAEGLYSIQGIFELKENDRIF <td>219</td>	219
DB <td>200 <td>-SCTNLPLSHKYMENSYPDQ</td></td>	200 <td>-SCTNLPLSHKYMENSYPDQ</td>	-SCTNLPLSHKYMENSYPDQ	

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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 108.052 Seconds
(without alignments)
869.796 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYKSGIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1287	100.0	279	2	AAW76332 Human TL2
2	1287	100.0	279	2	AAW95032 Tumour ne
3	1287	100.0	281	2	AAW19777 Novel cyt
4	1287	100.0	281	2	AAW27134 Human Apo
5	1287	100.0	281	2	AAW19787 Human apo
6	1287	100.0	281	2	AAW76829 Human TL2
7	1287	100.0	281	2	AAW56760 Human TRA
8	1287	100.0	281	2	AAW44354 Human AGP
9	1287	100.0	281	2	AAW01517 Protein a
10	1287	100.0	281	2	AAW27012 Human Apo
11	1287	100.0	281	3	AAW81956 Human PRO
12	1287	100.0	281	3	AAW24038 Human PRO
13	1287	100.0	281	3	AAW08545 Amino aci
14	1287	100.0	281	3	AAW28691 Human AGP
15	1287	100.0	281	4	AAW50977 Human PRO
16	1287	100.0	281	4	AAW67243 Human Apo
17	1287	100.0	281	4	AAW11031 Human TNF
18	1287	100.0	281	4	AAW48350 Human TL2
19	1287	100.0	281	5	AAW08133 Human TRA
20	1287	100.0	281	5	AAW31630 Human TRA
21	1287	100.0	281	5	AAW75062 Human TNF
22	1287	100.0	281	5	AAW51077 Human Apo
23	1287	100.0	281	5	AAW51954 Human Apo
24	1287	100.0	281	5	AAW19095 C neoform
25	1287	100.0	281	5	AAW79593 Human TNF

26	1287	100.0	281	6	ABG73861 Human Apo
27	1287	100.0	281	6	ABU10205 Human Apo
28	1287	100.0	281	6	ABU71443 Human neo
29	1287	100.0	281	6	ABG72738 Human TNF
30	1287	100.0	281	6	AAO29543 Human TRA
31	1287	100.0	281	6	ABU08558 Human TNF
32	1287	100.0	281	6	ABR42313 Human TRA
33	1287	100.0	281	6	ABG71905 Human TRA
34	1287	100.0	281	6	ABP60546 Human tum
35	1287	100.0	281	6	AAE36258 Human TR4
36	1287	100.0	281	6	AAO31151 Human TNF
37	1287	100.0	281	6	ABO25125 Human TNF
38	1287	100.0	281	7	ADB61471 Native hu
39	1287	100.0	281	7	ADC35202 Human TNF
40	1287	100.0	281	7	ADD14080 Human src
41	1287	100.0	281	7	ADD19010 Human dis
42	1287	100.0	281	7	ABW02276 Human TRA
43	1287	100.0	281	8	ADE76953 Human pro
44	1287	100.0	281	8	ADK72311 Human Apo
45	1287	100.0	281	8	ADK72303 Human Apo

ALIGNMENTS

RESULT 1

AAW76332

ID AAW76332 standard; protein; 279 AA.

XX AC AAW76332;

XX DT 11-JAN-1999 (first entry)

XX DE Human TL2 (TRAIL), ligand for TR5.

XX KW TL2; TRAIL; tumour necrosis related receptor; TR5; inflammation;

XX KW arthritis; septicemia; transplant rejection; autoimmune disease;

XX KW inflammatory bowel disease; graft versus host disease; infection; stroke;

XX KW ischaemia; acute respiratory disease syndrome; psoriasis; restenosis;

XX KW brain injury; AIDS; bone disease; cancer; atherosclerosis;

XX KW Alzheimer's disease; human; therapy; diagnosis; ligand.

XX OS Homo sapiens.

XX PN EP867509-A2.

XX PD 30-SEP-1998.

XX PF 04-FEB-1998; 98EP-00300827.

XX PR 05-FEB-1997; 97US-00795910.

XX PR 28-JUL-1997; 97US-00901469.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Young PR, Tan KB, Truneh A, Lyn SDP;

XX DR WPI; 1998-497862/43.

XX PT New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent

PT and treat e.g. inflammation, arthritis, septicemia, autoimmune diseases,

PT infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury,

PT AIDS and bone diseases.

XX PS Disclosure; Page 17-18; 22pp; English.

XX CC This is the amino acid sequence of human TL2 (also known as TRAIL), which

CC has newly been discovered to be a ligand of human tumour necrosis related

CC receptor TR5 (see AAW76331). This TR5 polypeptide of the invention and

CC TL2 can be used in screening processes for compounds which bind the

CC receptor, or its ligand, and which activate (agonists) or inhibit

CC (antagonists) the receptor or TL2. Treatment of a subject with the need

CC to inhibit TR5 polypeptide activity comprises administering an antagonist

CC to the polypeptide, administering a nucleic acid that inhibits the
CC expression of the nucleotide sequence encoding the polypeptide and/or
CC administering a polypeptide that competes with the polypeptide for its
CC ligand, substrate or receptor. The active agents can be used for the
CC treatment of chronic and acute inflammation, arthritis, septicemia,
CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),
CC transplant rejection, graft vs host disease, infection, stroke,
CC ischemia, acute respiratory disease syndrome, restenosis, brain injury,
CC AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders),
CC atherosclerosis and Alzheimer's disease
XX
SQ Sequence 279 AA;

Query Match 100.0%; Score 1287; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 3.4e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
DB 37 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 96
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 97 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 156
QY 121 SGHSFSLNHLRNGELVTHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 180
DB 157 SGHSFSLNHLRNGELVTHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 216
QY 181 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 217 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276
QY 241 LVG 243
DB 277 LVG 279

RESULT 2
ID AAW95032 standard; protein; 279 AA.
XX AAW95032;
AC
XX
DT 13-MAY-1999 (first entry)
XX
DE Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.
XX
KW Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;
KW inflammation; septicemia; autoimmune disease; transplant rejection;
KW graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
KW acute respiratory disease syndrome; restenosis; bone disease; cancer;
KW atherosclerosis; Alzheimer's disease.
XX
OS Unidentified.
XX
PN EP897114-A2.
XX
PD 17-FEB-1999.
XX
PF 04-JUN-1998; 98EP-00304424.
XX
PR 13-AUG-1997; 97US-0055513P.
PR 26-AUG-1997; 97US-0056980P.
PR 29-AUG-1997; 97US-0057550P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Brigham-Burke MR, Young PR;
XX
DR WPI; 1999-134308/12.
XX
PT Identifying agonists and antagonists to tumour necrosis factor receptor

PT (TNF-R) related polypeptides (LR1, LR2, LT2 and LT4) - useful for
PT treating stroke, Alzheimer's disease and AIDS.
XX
PS Disclosure; Page 14-15; 18pp; English.
XX
CC The invention relates to identifying agonists or antagonists to tumour
CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
CC candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2
CC or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)
CC assessing the ability of the candidate compound to compete with TR1 or
CC TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful
CC for treating diseases caused by imbalance of TL or TR polypeptide levels,
CC which cause: chronic and acute inflammation, arthritis, septicemia,
CC autoimmune diseases, transplant rejection, graft vs. host disease,
CC infection, stroke, ischemia, acute respiratory disease syndrome,
CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and
CC Alzheimer's disease. The present sequence represents a TNF-R related
CC polypeptide TL2
XX
SQ Sequence 279 AA;

Query Match 100.0%; Score 1287; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 3.4e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
DB 37 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 96
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 97 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 156
QY 121 SGHSFSLNHLRNGELVTHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 180
DB 157 SGHSFSLNHLRNGELVTHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 216
QY 181 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 217 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276
QY 241 LVG 243
DB 277 LVG 279

RESULT 3
AAW19777
ID AAW19777 standard; protein; 281 AA.
XX AAW19777;
AC AAW19777;
XX 22-SEP-1997 (first entry)
DT
XX
DE Novel cytokine Apo-2 ligand.
XX
KW Apo-2 ligand; cytokine; apoptosis; restenosis; breast cancer; colon cancer; therapy.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide 1..281
FT Region 1..14
FT Protein 15..281
FT Region 15..40
FT Protein 41..281
FT Region 41..281
Location/Qualifiers
/note= "Claim 4"
/label= Cytoplasmic_region
/note= "Claim 3"
/label= Transmembrane_region
/note= "Claim 2"

FT	Modified-site	/label= Extracellular_region	FT	Modified-site	/label= Extracellular_region
FT	109	/label= Glycosylation	FT	109	/label= Glycosylation
FT	114	/note= "putative N-linked glycosylation site"	FT	114	/note= "putative N-linked glycosylation site"
FT	281		FT	281	
FT	281	/note= "Claim 1"	FT	281	/note= "Claim 1"
XX			XX		
XX	WO9725428-A1.		XX	WO9725428-A1.	
XX	17-JUL-1997.		XX	17-JUL-1997.	
XX			XX		
XX	08-JAN-1997;	97WO-US000272.	XX	08-JAN-1997;	97WO-US000272.
XX			XX		
XX	09-JAN-1996;	96US-00584031.	XX	09-JAN-1996;	96US-00584031.
XX			XX		
XX	(GETH) GENENTECH INC.		XX	(GETH) GENENTECH INC.	
XX			XX		
XX	Ashkenazi AJ, Chuntharapai A, Kim KJ;		XX	Ashkenazi AJ, Chuntharapai A, Kim KJ;	
XX			XX		
XX	WPI; 1997-372867/34.		XX	WPI; 1997-372867/34.	
XX	N-PSDB; AAT72796.		XX	N-PSDB; AAT72796.	
XX			XX		
XX	Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce		XX	Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce	
XX	apoptosis for the treatment of breast and colon cancer.		XX	apoptosis for the treatment of breast and colon cancer.	
XX			XX		
XX	Claim 4; Fig 1a; 72pp; English.		XX	Claim 4; Fig 1a; 72pp; English.	
XX			XX		
XX	A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian		XX	A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian	
XX	cell apoptosis. It is believed to be a member of the tumour necrosis		XX	cell apoptosis. It is believed to be a member of the tumour necrosis	
XX	factor cytokine family. Its amino acid sequence was deduced from a cDNA		XX	factor cytokine family. Its amino acid sequence was deduced from a cDNA	
XX	clone (AAT72796) isolated from a human placental cDNA library. Apo-2		XX	clone (AAT72796) isolated from a human placental cDNA library. Apo-2	
XX	ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-		XX	ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-	
XX	281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells		XX	281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells	
XX	transformed or transfected with a vector contg. Apo-2 ligand nucleic		XX	transformed or transfected with a vector contg. Apo-2 ligand nucleic	
XX	acid. They can be used to induce apoptosis in mammals and to treat		XX	acid. They can be used to induce apoptosis in mammals and to treat	
XX	pathological conditions such as cancer (esp. breast or colon cancer) or		XX	pathological conditions such as cancer (esp. breast or colon cancer) or	
XX	to raise antibodies useful in diagnostic assays		XX	to raise antibodies useful in diagnostic assays	
XX			XX		
XX	Sequence 281 AA;		XX	Sequence 281 AA;	
XX			XX		
XX	Query Match	100.0%; Score 1287; DB 2; Length 281;	XX	Query Match	100.0%; Score 1287; DB 2; Length 281;
XX	Best Local Similarity	100.0%; Pred. No. 3.4e-117;	XX	Best Local Similarity	100.0%; Pred. No. 3.4e-117;
XX	Matches 243; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	XX	Matches 243; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	TNELKQMDKYSKSGIACFLKEDDSYWPNDDESMNSPCWQVKQLRLVRKMLRTSEE 60	QY	1	TNELKQMDKYSKSGIACFLKEDDSYWPNDDESMNSPCWQVKQLRLVRKMLRTSEE 60
DB	39	TNELKQMDKYSKSGIACFLKEDDSYWPNDDESMNSPCWQVKQLRLVRKMLRTSEE 98	DB	39	TNELKQMDKYSKSGIACFLKEDDSYWPNDDESMNSPCWQVKQLRLVRKMLRTSEE 98
QY	61	TISTVQEKQONISPLVRERGPORVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 120	QY	61	TISTVQEKQONISPLVRERGPORVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 120
DB	99	TISTVQEKQONISPLVRERGPORVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 158	DB	99	TISTVQEKQONISPLVRERGPORVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 158
QY	121	SGHSFSLNHLRNGELVITHEKGFYIYSQTYPRFOEIKENTKNDKQMVQIYKYTSYDP 180	QY	121	SGHSFSLNHLRNGELVITHEKGFYIYSQTYPRFOEIKENTKNDKQMVQIYKYTSYDP 180
DB	159	SGHSFSLNHLRNGELVITHEKGFYIYSQTYPRFOEIKENTKNDKQMVQIYKYTSYDP 218	DB	159	SGHSFSLNHLRNGELVITHEKGFYIYSQTYPRFOEIKENTKNDKQMVQIYKYTSYDP 218
QY	181	PILLMKARSNCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240	QY	181	PILLMKARSNCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB	219	PILLMKARSNCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278	DB	219	PILLMKARSNCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY	241	LVG 243	QY	241	LVG 243
DB	279	LVG 281	DB	279	LVG 281
XX			XX		
XX	RESULT 4		XX	RESULT 4	
XX	AAW27134		XX	AAW27134	
XX	AAW27134 standard; protein; 281 AA.		XX	AAW27134 standard; protein; 281 AA.	
XX			XX		
XX	AAW27134;		XX	AAW27134;	
XX			XX		
XX	02-APR-1998 (first entry)		XX	02-APR-1998 (first entry)	
XX			XX		

```

RESULT 5
AAW19787
ID AAW19787 standard; protein; 281 AA.
XX
AC AAW19787;
XX
DT 24-SEP-1997 (first entry)
XX
DE Human apoptosis inducer cytokine TRAIL.
XX
KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
KW thrombotic microangioplasty; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..118 /label= Cytoplasmic_domain
FT Domain 19..38 /label= Transmembrane_domain
FT Domain 39..281 /label= Extracellular_domain
FT /note= "contains a receptor-binding region"
FT Cleavage-site 89..90 /note= "potential KEX2 protease processing site"
FT Modified-site 109..111 /note= "potential N-glycosylation site"
FT Cleavage-site 149..150 /note= "potential KEX2 protease processing site"
FT
FT
PN WO9701633-A1.
XX
XX 16-JAN-1997.
XX
XX 25-JUN-1996; 96WO-US010895.
XX
XX 29-JUN-1995; 95US-00496632.
XX 01-NOV-1995; 95US-00548368.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Wiley SR, Goodwin RG;
XX
XX WPI; 1997-118715/11.
XX N-PSDB; AAT72847.
XX
XX TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
XX cells - useful for treating thrombotic microangiopathy, cancer and viral
XX infection and for use in assays.
XX
XX Claim 10; Page 43-44; 62pp; English.
XX
XX Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
XX (AAW19787) is a novel cytokine that induces apoptosis of certain target
XX cells, including cancer cells and virally infected cells. Its amino acid
XX sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in
XX vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
XX polypeptides) can be expressed in host cells and used in the treatment of
XX cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
XX to raise antibodies that may be useful for treating thrombotic
XX microangiopathies
XX
XX Sequence 281 AA;
XX
Query Match 100.0%; Score 1287; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.4e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQLRKMLRTSSE 60
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQLRKMLRTSSE 98
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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QY 61 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
|||
DB 99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
|||
QY 121 SGHSFLSNLHLRNGELVTHEKGFYIYSOTYFRFOSEIKENTKNDKQWQYIYKYTSYPD 180
|||
DB 159 SGHSFLSNLHLRNGELVTHEKGFYIYSOTYFRFOSEIKENTKNDKQWQYIYKYTSYPD 218
|||
QY 181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
|||
DB 219 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
|||
QY 241 LVG 243
|||
DB 279 LVG 281
|||

RESULT 6
AAW76829
ID AAW76829 standard; protein; 281 AA.
XX
AC AAW76829;
XX
DT 25-JAN-1999 (first entry)
XX
DE Human TL2 protein.
XX
KW TR6; tumour necrosis factor related receptor; human; treatment; stroke;
KW inflammation; arthritis; septicaemia; autoimmune disease; restenosis;
KW transplant rejection; infection; ischaemia; brain injury; bone disease;
KW acute respiratory disease syndrome; acquired autoimmune disease syndrome;
KW AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF;
KW TL2. tumour necrosis factor-related apoptosis-inducing ligand.
XX
OS Homo sapiens.
XX
XX EP870827-A2.
XX
XX 14-OCT-1998.
XX
XX 23-DEC-1997; 97EP-00310562.
XX
XX 14-MAR-1997; 97US-0041230P.
XX 09-MAY-1997; 97US-00853684.
XX 22-AUG-1997; 97US-00916625.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Deen KC, Young PR;
XX
XX WPI; 1998-523156/45.
XX N-PSDB; AAV63096.
XX
XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding
XX polypeptide, antibody, agonist, antagonist, etc.
XX
XX Disclosure; Page 32-33; 34pp; English.
XX
XX This sequence represents the human tumour necrosis factor (TNF)-related
XX receptor, TL2 (also known as tumour necrosis factor-related apoptosis-
XX inducing ligand, TRAIL). This protein is used in a method resulting in
XX the isolation of the novel human TNF related receptor, TR6. TR6
XX polypeptides and polynucleotides can be used in the treatment of chronic
XX and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g.
XX inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
XX host disease, infection, stroke, ischaemia, acute respiratory disease
XX syndrome, restenosis, brain injury, (acquired autoimmune disease
XX syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative
XX disorders), atherosclerosis and Alzheimers disease
XX
XX Sequence 281 AA;
XX
Query Match 100.0%; Score 1287; DB 2; Length 281;

```


CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
 CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
 CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or
 CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,
 CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat
 CC haematopoietic diseases associated with reduction in the number of bone
 CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
 CC by disease, injury or exposure to myelosuppressive agents. Host cells,
 CC transformed with expression vectors containing AGP-1 DNA, are used to
 CC produce recombinant AGP-1
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.4e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98
 QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHLRNGELVIEHKGFFYIYSQTYPRFOEIKENTKNDKQMVQYIYKYTSYDP 180
 DB 159 SGHSFLSNLHLRNGELVIEHKGFFYIYSQTYPRFOEIKENTKNDKQMVQYIYKYTSYDP 218
 QY 181 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281

RESULT 9
 AAY01517
 ID AAY01517 standard; peptide; 281 AA.

XX AC AAY01517;
 XX DT 27-MAY-1999 (first entry)
 XX DE Protein associated with neurodegenerative and autoimmune diseases.
 XX KW Neurodegenerative disease; autoimmune disease; inflammatory disease;
 XX KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
 XX KW surface receptor; TRAIL protein.

XX OS Homo sapiens.
 XX PN FR2766713-A1.
 XX PD 05-FEB-1999.
 XX PF 04-AUG-1997; 97FR-00010176.
 XX PR 04-AUG-1997; 97FR-00010176.
 XX PA (INMR) BIO MERIEUX.
 XX PI Rieger F, Belliveau JF, Perron H;
 XX DR WPI; 1999-156177/14.

XX Use of polypeptide derived from TRAIL protein for diagnosis of
 PT degenerative disease - autoimmunity and inflammation, also useful in
 PT prevention or treatment, and similar use of corresponding ligand and
 PT nucleic acid.

XX Claim 2; Page 13; 21pp; French.

XX The specification describes the use a polypeptide corresponding to at
 CC least the primary sequence of part of the present sequence to produce a
 CC diagnostic, prophylactic or therapeutic composition useful in cases of
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
 CC be used in treatment of neurodegenerative diseases, lupus erythematosus,
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
 CC nervous system cells, antigenic and specifically recognise the surface and
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
 CC receptors, inhibiting formation of natural complex

SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.4e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98
 QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHLRNGELVIEHKGFFYIYSQTYPRFOEIKENTKNDKQMVQYIYKYTSYDP 180
 DB 159 SGHSFLSNLHLRNGELVIEHKGFFYIYSQTYPRFOEIKENTKNDKQMVQYIYKYTSYDP 218
 QY 181 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281

RESULT 10
 AAY27012
 ID AAY27012 standard; protein; 281 AA.

XX AC AAY27012;
 XX DT 24-SEP-1999 (first entry)
 XX DE Human Apo-2 ligand (Apo-2L) polypeptide.
 XX KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
 XX KW lupus; immune-mediated glomerular nephritis; human.

XX OS Homo sapiens.
 XX PN WO9936535-A1.
 XX PD 22-JUL-1999.
 XX PF 15-JAN-1999; 99WO-US001039.
 XX PR 15-JAN-1998; 98US-00007886.
 XX PR 15-APR-1998; 98US-00060533.
 XX PA (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;
 XX WPI; 1999-444397/37.
 XX DR N-PSDB; AAX86987.

PT A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 PT in mammalian cancer cells.
 XX Claim 1; Fig 1A; 86pp; English.

XX This sequence represents a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis
 XX

XX Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.4e-117; Mismatches 0; Indels 0; Gaps 0;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEE 98
 QY 61 TISTVQEKQONISPLVRERGQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQONISPLVRERGQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 180
 DB 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 218
 QY 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281

RESULT 11
 ID AAY81956
 AC AAY81956;
 DT 10-JUL-2000 (first entry)
 DE Human Apo-2 ligand protein sequence.
 DE Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
 KW therapy; apoptosis; cancer.
 KW

XX Homo sapiens.
 XX US6046048-A.
 XX 04-APR-2000.
 XX 08-JAN-1997; 97US-00780496.
 XX 09-JAN-1996; 96US-0009755P.
 XX (GETH) GENENTECH INC.
 XX Kim KJ, Ashkenazi AJ, Chuntharapai A;
 PI WPI; 2000-282690/24.
 DR N-PSDB; AAA07425.
 XX

PT New isolated monoclonal antibodies having antigen specificity for Apo-2
 PT ligand, e.g. 2E11 or 5C2, useful for detecting the expression of Apo
 PT -2 ligand serum, and for treating diseases associated with increased
 PT apoptosis.

XX Claim 9; Fig 1A; 46pp; English.

XX This sequence is the human Apo-2 ligand protein, which is recognised by
 CC monoclonal antibodies produced by the hybridoma cell lines of the
 CC invention. The hybridoma cell lines are deposited under the American Type
 CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
 CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
 CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
 CC tissues, or serum. The antibodies may also be employed as therapeutics.
 CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
 CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
 CC pathological conditions or diseases associated with increased apoptosis.
 CC They are also useful for the affinity purification of Apo-2 ligand from
 CC recombinant cell culture or natural sources. The Apo-2 ligand itself may
 CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells
 CC

XX Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.4e-117; Mismatches 0; Indels 0; Gaps 0;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEE 98
 QY 61 TISTVQEKQONISPLVRERGQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQONISPLVRERGQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 180
 DB 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 218
 QY 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281

RESULT 12
 ID AAB24038
 AC AAB24038;
 DT 25-JAN-2001 (first entry)
 DE Human PRO1096 protein sequence SEQ ID NO:51.

XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 KW identification; tumourigenesis; anticancer; detection.
 KW

OS Homo sapiens.
 XX WO200053750-A1.
 XX 14-SEP-2000.
 XX 02-DEC-1999; 99WO-US028551.
 XX 08-MAR-1999; 99WO-US005028.
 XX 01-SEP-1999; 99WO-US020111.
 XX 28-OCT-1999; 99US-0162506P.
 XX 30-NOV-1999; 99WO-US028313.

PR	01-DEC-1999;	99WO-US028634.	
XX	(GETH)	GENENTECH INC.	
PA	Botstein D,	Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;	
XX	PI		
XX	WPI; 2000-594320/56.		
DR	DR	N-PSDB; AAC58120.	
XX	XX		
XX	Antibodies specific for PRO polypeptides, used to diagnose and inhibit		
PT	the growth of tumors in mammals, and to identify inhibitors of PRO		
PT	polypeptide activity or expression.		
XX	XX		
PS	Claim 61; Fig 36; 226pp; English.		
XX	XX		
CC	The present invention describes an antibody that binds to a human protein		
CC	(I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;		
CC	PRO1927; PRO3567; PRO1295; PRO1303; PRO4344; PRO4354; PRO4397;		
CC	PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer		
CC	activity and can be used to diagnose tumours in mammals, by detecting		
CC	complex formation when the antibody is contacted with test cells.		
CC	Increased expression of genes encoding (I) can also be detected to		
CC	diagnose tumours. Agents which inhibit the activity of (I), especially		
CC	the antibodies, or an antisense oligonucleotide which hybridises to genes		
CC	encoding (I), can be used to inhibit tumour growth, preferably by		
CC	inducing cell death. Methods from the present invention can be used to		
CC	identify compounds which inhibit the biological activity of (I). AAC58019		
CC	to AAC58102 represent PCR primers and hybridisation probes used in		
CC	examples from the present invention for human PRO sequences. AAC58103 to		
CC	AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and		
CC	protein sequences given in the exemplification of the present invention		
XX	XX		
SQ	Sequence 281 AA;		
Query Match 100.0%; Score 1287; DB 3; Length 281;			
Best Local Similarity 100.0%; Pred. No. 3.4e-117;			
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMSPCQVKWQRLVRKMLRTSEE 60	
Db	39	TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMSPCQVKWQRLVRKMLRTSEE 98	
QY	61	TISTVQEKQONISPLVRERGQORVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 120	
Db	99	TISTVQEKQONISPLVRERGQORVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 158	
QY	121	SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKTSYPD 180	
Db	159	SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKTSYPD 218	
QY	181	PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240	
Db	219	PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278	
QY	241	LVG 243	
Db	279	LVG 281	
RESULT 13			
AAB08545			
ID	AAB08545	standard; protein; 281 AA.	
XX	XX		
AC	AAB08545;		
XX	XX		
DT	20-DEC-2000	(first entry)	
XX	XX		
DE	Amino acid sequence of a human TRAIL polypeptide.		
XX	XX		
KW	Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;		
KW	TNF related apoptosis-inducing ligand; tumour cell;		
KW	TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;		
KW	non-small cell lung carcinoma.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
PN	WO200048619-A1.		
XX	XX		
PD	24-AUG-2000.		
XX	XX		
PF	15-FEB-2000; 2000WO-US003891.		
XX	XX		
PR	16-FEB-1999; 99US-0120313P.		
XX	XX		
PA	(STRD) UNIV LELAND STANFORD JUNIOR.		
XX	XX		
PI	Rosen GD;		
XX	XX		
DR	WPI; 2000-558253/51.		
DR	N-PSDB; AAA64325.		
XX	XX		
PT	Killing of tumor cells, e.g. solid tumors or carcinoma, comprises		
PT	administration of synergistic combination of diterpenoid diepoxide and		
PT	tumor necrosis factor related apoptosis-inducing ligand.		
XX	XX		
PS	Disclosure; Page 23-24; 29pp; English.		
XX	XX		
CC	The present sequence represents a human TRAIL (tumour necrosis factor		
CC	(TNF) related apoptosis-inducing ligand) polypeptide. The specification		
CC	describes a method for enhanced killing of tumour cells. The method		
CC	comprises contacting a susceptible tumour cell with a synergistic mixture		
CC	of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined		
CC	dosage to kill at least 50 % of the cells. This mixture is synergistic,		
CC	and so is active at lower doses and against otherwise resistant cell		
CC	lines. The method is used for killing tumour cells, especially solid		
CC	tumours or carcinomas (especially mammary carcinoma or non-small cell		
CC	lung carcinoma)		
XX	XX		
SQ	Sequence 281 AA;		
Query Match 100.0%; Score 1287; DB 3; Length 281;			
Best Local Similarity 100.0%; Pred. No. 3.4e-117;			
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMSPCQVKWQRLVRKMLRTSEE 60	
Db	39	TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMSPCQVKWQRLVRKMLRTSEE 98	
QY	61	TISTVQEKQONISPLVRERGQORVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 120	
Db	99	TISTVQEKQONISPLVRERGQORVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 158	
QY	121	SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKTSYPD 180	
Db	159	SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKTSYPD 218	
QY	181	PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240	
Db	219	PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278	
QY	241	LVG 243	
Db	279	LVG 281	
RESULT 14			
AAB28691			
ID	AAB28691	standard; protein; 281 AA.	
XX	XX		
AC	AAB28691;		
XX	XX		
DT	14-FEB-2001	(first entry)	
XX	XX		
DE	Human AGP-1.		
XX	XX		
KW	Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;		

Db	39	TNELKOMQDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILTSEE	98
Qy	61	TTSTVOEKQONTISPLVREGRGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	120
Db	99	TTSTVOEKQONTISPLVREGRGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	158
Qy	121	SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD	180
Db	159	SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD	218
Qy	181	PILLMKSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	240
Db	219	PILLMKSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	278
Qy	241	LVG	243
Db	279	LVG	281

Search completed: June 22, 2005, 06:07:14
Job time : 109.052 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:01:21 ; Search time 564.372 Seconds
(without alignments)
165.329 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287
Sequence: 1 TNELKMDKYSKGTACFL.....NEHLMDHDSFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1287	100.0	281	8	US-08-916-625B-6
3	1287	100.0	281	8	US-08-971-317A-8
4	1287	100.0	281	9	US-09-813-329-17
5	1287	100.0	281	9	US-09-393-663-8
6	1287	100.0	281	9	US-09-934-465-1
7	1287	100.0	281	10	US-09-919-039-118
8	1287	100.0	281	13	US-10-011-125-4
9	1287	100.0	281	13	US-10-001-054-54
10	1287	100.0	281	14	US-10-093-766-54
11	1287	100.0	281	14	US-10-174-654-11

12	1287	100.0	281	14	US-10-151-882-41	Sequence 41, Appl
13	1287	100.0	281	14	US-10-218-547-20	Sequence 20, Appl
14	1287	100.0	281	14	US-10-322-673-72	Sequence 72, Appl
15	1287	100.0	281	14	US-10-139-785-66	Sequence 66, Appl
16	1287	100.0	281	14	US-10-310-793-26	Sequence 26, Appl
17	1287	100.0	281	15	US-10-279-687-8	Sequence 8, Appl
18	1287	100.0	281	15	US-10-292-486-5	Sequence 5, Appl
19	1287	100.0	281	15	US-10-333-712-1	Sequence 1, Appl
20	1287	100.0	281	15	US-10-662-429-2	Sequence 20, Appl
21	1287	100.0	281	15	US-10-202-062-20	Sequence 20, Appl
22	1287	100.0	281	15	US-10-662-431-2	Sequence 2, Appl
23	1287	100.0	281	15	US-10-662-430-2	Sequence 2, Appl
24	1287	100.0	281	15	US-10-652-244-2	Sequence 2, Appl
25	1287	100.0	281	15	US-10-381-160-5	Sequence 5, Appl
26	1287	100.0	281	16	US-10-755-889-210	Sequence 210, App
27	1287	100.0	281	16	US-10-491-326-1	Sequence 1, Appl
28	1287	100.0	281	16	US-10-810-063-2	Sequence 2, Appl
29	1287	100.0	281	16	US-10-825-282-22	Sequence 22, Appl
30	1287	100.0	281	16	US-10-825-282-24	Sequence 24, Appl
31	1287	100.0	281	16	US-10-393-116-5	Sequence 5, Appl
32	1287	100.0	281	16	US-10-688-845-36	Sequence 36, Appl
33	1287	100.0	281	16	US-10-861-685-1	Sequence 1, Appl
34	1287	100.0	281	17	US-10-771-254-1	Sequence 1, Appl
35	1287	100.0	281	17	US-10-855-559-2	Sequence 2, Appl
36	1287	100.0	281	17	US-10-451-200-5	Sequence 5, Appl
37	1287	100.0	281	17	US-10-495-353-1	Sequence 1, Appl
38	1287	100.0	281	17	US-10-652-979-1	Sequence 1, Appl
39	1282	99.6	266	16	US-10-738-423-10	Sequence 10, Appl
40	1265	98.3	279	16	US-10-367-094-22	Sequence 22, Appl
41	1246	96.8	283	17	US-10-978-203-23	Sequence 23, Appl
42	1246	96.8	283	17	US-10-978-131-23	Sequence 23, Appl
43	1078.5	83.8	246	9	US-09-855-544A-13	Sequence 13, Appl
44	1047	81.4	271	16	US-10-781-866-30	Sequence 30, Appl
45	997.5	77.5	400	16	US-10-723-003-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-10-066-209-3
; Sequence 3, Application US/10066209
; Publication No. US2002015110A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: CH-50030-D1
; CURRENT APPLICATION NUMBER: US/10/066,209
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/072,993
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-066-209-3

Query Match 100.0%; Score 1287; DB 13; Length 279;
Best Local Similarity 100.0%; Pred. NO. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKMDKYSKGTACFLKEDDSYWDNDESNMSPCWKQWOLRQVLRKMLTSEE 60
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Db 37 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCQVKWQRLQRLVRKMLTSEE 96
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Db 97 T1STVQEKQONTISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 156
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Db 157 SGHSFLSNLHNLRLNGELVIEHKGFFYYISQTYPRFQEEIKENTKNDKQMVQYIYKYTSYD 216
QY 181 PILLKMSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 240
Db 217 PILLKMSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 276
QY 241 LVG 243
Db 277 LVG 279

RESULT 2
US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Publication No. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; TITLE OF INVENTION: RECEPTOR, TR6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50008-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846189
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-916-625B-6
Query Match 100.0%; Score 1287; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCQVKWQRLQRLVRKMLTSEE 60
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Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCQVKWQRLQRLVRKMLTSEE 98
QY 61 T1STVQEKQONTISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 T1STVQEKQONTISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHNLRLNGELVIEHKGFFYYISQTYPRFQEEIKENTKNDKQMVQYIYKYTSYD 180
Db 159 SGHSFLSNLHNLRLNGELVIEHKGFFYYISQTYPRFQEEIKENTKNDKQMVQYIYKYTSYD 218
QY 181 PILLKMSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 240
Db 219 PILLKMSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 3
US-08-971-317A-8
; Sequence 8, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,317A
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mimi C
; REGISTRATION NUMBER: 39,046
; REFERENCE/DOCKET NUMBER: 6255.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-8

Query Match 100.0%; Score 1287; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCQVKWQRLQRLVRKMLTSEE 60
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Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCQVKWQRLQRLVRKMLTSEE 98
|||||
QY 61 T1STVQEKQONTISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
|||||

Db 99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMWQYIYKYTSYDP 180
Db 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMWQYIYKYTSYDP 218
QY 181 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASPPGAF 240
Db 219 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASPPGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 4

US-09-813-329-17
; Sequence 17, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-17

Query Match 100.0%; Score 1287; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCWQVQWLQRLVKRMILRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCWQVQWLQRLVKRMILRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMWQYIYKYTSYDP 180
Db 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMWQYIYKYTSYDP 218
QY 181 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASPPGAF 240
Db 219 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASPPGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 5

US-09-193-663-8
; Sequence 8, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.02
; CURRENT APPLICATION NUMBER: US/09/193,663
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916

; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-8

Query Match 100.0%; Score 1287; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCWQVQWLQRLVKRMILRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCWQVQWLQRLVKRMILRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMWQYIYKYTSYDP 180
Db 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMWQYIYKYTSYDP 218
QY 181 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASPPGAF 240
Db 219 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASPPGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 6

US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. US2002010233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match 100.0%; Score 1287; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCWQVQWLQRLVKRMILRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCWQVQWLQRLVKRMILRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMWQYIYKYTSYDP 180
Db 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMWQYIYKYTSYDP 218
QY 181 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASPPGAF 240
Db 219 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASPPGAF 278

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QY 241 LVG 243
Db 279 LVG 281

RESULT 7
US-09-919-039-118
; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaer, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118

Query Match 100.0%; Score 1287; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGIACFLKEDDSYWDPNDESNNPCWQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGIACFLKEDDSYWDPNDESNNPCWQVKWQLRQLVRKMLRTSEE 98
QY 61 TTSTVQEKQNTISPLVREGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TTSTVQEKQNTISPLVREGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQMVQYIYKTSYDP 180
Db 159 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQMVQYIYKTSYDP 218
QY 181 PILLKMSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLKMSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 9
US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Shelton, David
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/096891
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/096894
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100263
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: 60/100390

QY 1 TNELKQMDKYSGIACFLKEDDSYWDPNDESNNPCWQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGIACFLKEDDSYWDPNDESNNPCWQVKWQLRQLVRKMLRTSEE 98
QY 61 TTSTVQEKQNTISPLVREGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TTSTVQEKQNTISPLVREGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQMVQYIYKTSYDP 180
Db 159 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQMVQYIYKTSYDP 218
QY 181 PILLKMSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLKMSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 8
US-10-011-125-4
; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4
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;
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/107783
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112420
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/115554
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116533
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/131294
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/218517
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/284291
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380913
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 09/403297
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/423741
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/802706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/866034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/882636
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28

;
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US99/00106
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/08615
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28634
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00376
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/06884
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/13705
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/14941
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/22031
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US01/27099
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 91

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; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-54

Query Match      100.0%; Score 1287; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDSDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDSDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVREGPQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGPQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQBEIKENTKNDKQMVQYIYKYTSYDP 180
Db 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQBEIKENTKNDKQMVQYIYKYTSYDP 218

QY 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
Db 279 LVG 281

RESULT 10
US-10-093-766-54
; Sequence 54, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Laesk, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54
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Query Match      100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDSDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDSDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVREGPQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGPQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQBEIKENTKNDKQMVQYIYKYTSYDP 180
Db 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQBEIKENTKNDKQMVQYIYKYTSYDP 218

QY 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
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QY 241 LVG 243
Db 279 LVG 281

RESULT 11
US-10-174-654-11
; Sequence 11, Application US/10174654
; Publication No. US20030044937A1
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pharmacia & Upjohn, Intellectual Property
; CITY: Kalamazoo
; STREET: 301 Henrietta Street
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/174,654
; FILING DATE: 19-Jun-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-174-654-11
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Query Match      100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDSDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDSDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVREGPQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGPQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQBEIKENTKNDKQMVQYIYKYTSYDP 180
Db 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQBEIKENTKNDKQMVQYIYKYTSYDP 218

QY 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
Db 279 LVG 281
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Query Match	100.0%;	Score 1287;	DB 14;	Length 281;
Best Local Similarity	100.0%;	Pred. No. 1e-110;		
Matches	243;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
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Db	39	TNELQMODKYKSGIACFLKEDDSYWPNDDEESNNSPCQVWKQLRQLVRKMLRTSEE	98	
Qy	61	T1STVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	120	
Db	99	T1STVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	158	
Qy	121	SGHSFLSNLHLRANGELVTHEKGFYIYSQTYFRQOEIKENTKNDKQMWQVYKYTSPD	180	
Db	159	SGHSFLSNLHLRANGELVTHEKGFYIYSQTYFRQOEIKENTKNDKQMWQVYKYTSPD	218	
Qy	181	PILLMKSARNSCWSKDAEYGLYSIYQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAF	240	
Db	219	PILLMKSARNSCWSKDAEYGLYSIYQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAF	278	

QY 241 LVG 243
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Db 279 LVG 281

RESULT 15
US-10-139-785-66
; Sequence 66, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-66

Query Match 100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYD 180
Db 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYD 218
QY 181 PILLMKSARNCSWKAEGYLSIYQGGIFELKENDRIFVSVTNEHLIDMDHEADSPFGAF 240
Db 219 PILLMKSARNCSWKAEGYLSIYQGGIFELKENDRIFVSVTNEHLIDMDHEADSPFGAF 278
QY 241 LVG 243
|||
Db 279 LVG 281

Search completed: June 22, 2005, 06:39:14
Job time : 565.372 secs

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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 27.8244 Seconds
(without alignments)
651.935 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYSKSGIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1287	100.0	279	3	US-09-072-993C-3
2	1287	100.0	281	1	US-08-670-354-2
3	1287	100.0	281	3	US-08-584-031-1
4	1287	100.0	281	3	US-08-780-496-1
5	1287	100.0	281	3	US-08-883-086-10
6	1287	100.0	281	3	US-09-320-424-2
7	1287	100.0	281	3	US-09-333-593A-6
8	1287	100.0	281	4	US-09-157-864-11
9	1287	100.0	281	4	US-09-825-563-2
10	1287	100.0	281	4	US-09-919-039-118
11	1287	100.0	281	4	US-09-582-450-1
12	1287	100.0	281	4	US-09-934-465-1
13	1287	100.0	281	4	US-10-011-125A-4
14	1287	100.0	281	5	PCT-US96-10895-2
15	1047	81.4	271	4	US-09-569-611C-30
16	988	76.8	253	3	US-09-320-424-11
17	988	76.8	253	3	US-09-825-563-11
18	988	76.8	256	3	US-09-320-424-13
19	988	76.8	256	4	US-09-825-563-13
20	930	72.3	177	3	US-09-105-343A-7
21	863	67.1	291	1	US-08-670-354-6
22	863	67.1	291	3	US-09-320-424-6
23	863	67.1	291	4	PCT-US96-10895-6
24	863	67.1	291	5	PCT-US96-10895-6
25	850	66.0	161	4	US-09-565-423-7
26	544	50.8	183	3	US-09-105-343A-8
27	544	42.3	169	4	US-09-569-611C-29

28	446	34.7	85	4	US-09-632-287A-12	Sequence 12, Appl
29	425	33.0	121	4	US-09-513-999C-7833	Sequence 7833, Ap
30	292	22.7	120	4	US-09-569-611C-32	Sequence 32, Appl
31	291	22.6	101	1	US-08-670-354-4	Sequence 4, Appl
32	291	22.6	101	3	US-09-320-424-4	Sequence 4, Appl
33	291	22.6	101	4	US-09-825-563-4	Sequence 4, Appl
34	291	22.6	101	5	PCT-US96-10895-4	Sequence 4, Appl
35	291	22.6	122	4	US-09-569-611C-31	Sequence 31, Appl
36	245.5	19.1	87	4	US-09-632-287A-13	Sequence 13, Appl
37	238.5	18.5	294	3	US-08-996-139-11	Sequence 11, Appl
38	238.5	18.5	294	3	US-08-995-659-11	Sequence 11, Appl
39	238.5	18.5	294	3	US-09-215-649A-11	Sequence 11, Appl
40	238.5	18.5	294	4	US-09-577-780-11	Sequence 11, Appl
41	238.5	18.5	294	4	US-09-577-800-11	Sequence 11, Appl
42	238.5	18.5	294	4	US-09-466-496-11	Sequence 11, Appl
43	238.5	18.5	294	4	US-09-871-856-11	Sequence 11, Appl
44	238.5	18.5	294	4	US-09-871-291-11	Sequence 11, Appl
45	238.5	18.5	294	4	US-09-877-650-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-072-993C-3

; Sequence 3, Application US/09072993C

; Patent No. 6346388

; GENERAL INFORMATION:

; APPLICANT: Michael R. Brigham-Burke

; APPLICANT: Peter R. Young

; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND

; FILE REFERENCE: GH-50030

; CURRENT APPLICATION NUMBER: US/09/072,993C

; CURRENT FILING DATE: 1998-05-06

; PRIOR APPLICATION NUMBER: 60/055,513

; PRIOR FILING DATE: 1997-08-13

; PRIOR APPLICATION NUMBER: 60/056,980

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/057,550

; PRIOR FILING DATE: 1997-08-29

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 279

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-072-993C-3

Query Match 100.0%; Score 1287; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.8e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TNELKQMDKYSKSGIACFLKDDSYDNDDESMNSPCWQVKWLQRLVKMLRTSEE	60
Db	37	TNELKQMDKYSKSGIACFLKDDSYDNDDESMNSPCWQVKWLQRLVKMLRTSEE	96
Qy	61	TISTVQEKQONISPLVRERGPQVAHAHTTGRSNTLSSPNSKNEKALGRKINSWESSR	120
Db	97	TISTVQEKQONISPLVRERGPQVAHAHTTGRSNTLSSPNSKNEKALGRKINSWESSR	156
Qy	121	SGHSFSLNHLRNGELVIEHKGPYYIYSQTYFRFOBEIKENTKNDKQVQYIYKTSYPD	180
Db	157	SGHSFSLNHLRNGELVIEHKGPYYIYSQTYFRFOBEIKENTKNDKQVQYIYKTSYPD	216
Qy	181	PILLMSARNSCWSKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	240
Db	217	PILLMSARNSCWSKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	276
Qy	241	LVG 243	
Db	277	LVG 279	

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RESULT 2
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

Query Match      100.0%; Score 1287; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYKSGIACFLKEDDSYDPNDEESMNSPCWQVKQLROLVRKMILRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYDPNDEESMNSPCWQVKQLROLVRKMILRTSEE 98

Qy 61 TISTVQEKQNI SPLVRERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQNI SPLVRERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHSFSLNHLRNGELVTHEKGFYIYSQTFPRQEEIKENTKNDKQMWQVIYKYTSYDP 180
Db 159 SGHSFSLNHLRNGELVTHEKGFYIYSQTFPRQEEIKENTKNDKQMWQVIYKYTSYDP 218

Qy 181 PILLMKSRNSCWSKDAEYGLYSYVQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSRNSCWSKDAEYGLYSYVQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Qy 241 LVG 243
Db 279 LVG 281

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-780-496-1

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDP 180
DB 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDP 218
QY 181 PILLMSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 5
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembaki, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134, US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
; US-08-883-086-10

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDP 180
DB 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDP 218
QY 181 PILLMSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 6
US-09-320-424-2
; Sequence 2, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-09-320-424-2

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
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Matches	243;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE	60						
Db	39	TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE	98						
Qy	61	TISTVQEKQONISPLVREGRQPQVAHIITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	120						
Db	99	TISTVQEKQONISPLVREGRQPQVAHIITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	158						
Qy	121	SGHSFSLNLHLRNGELVLIHEKGFYYIYSQTYPRFQBEIKENTKNDKQMVQYIYKYTSPD	180						
Db	159	SGHSFSLNLHLRNGELVLIHEKGFYYIYSQTYPRFQBEIKENTKNDKQMVQYIYKYTSPD	218						
Qy	181	PILLMKSARNCSWKSDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	240						
Db	219	PILLMKSARNCSWKSDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	278						
Qy	241	LVG 243							
Db	279	LVG 281							
RESULT 11									
US-09-582-450-1									
; Sequence 1, Application US/09582450									
; Patent No. 6740739									
; GENERAL INFORMATION:									
; APPLICANT: Ashkenazi, Avi J.									
; APPLICANT: Kelley, Robert F.									
; APPLICANT: O'Connell, Mark P.									
; APPLICANT: Pitti, Robert M.									
; APPLICANT: Schwall, Ralph H.									
; TITLE OF INVENTION: Apo-2 Ligand									
; FILE REFERENCE: P0978P4									
; CURRENT APPLICATION NUMBER: US/09/582,450									
; CURRENT FILING DATE: 2001-05-14									
; PRIOR APPLICATION NUMBER: US 09/007,886									
; PRIOR FILING DATE: 1998-01-15									
; PRIOR APPLICATION NUMBER: US 09/060,533									
; PRIOR FILING DATE: 1998-04-15									
; NUMBER OF SEQ ID NOS: 17									
; SEQ ID NO 1									
; LENGTH: 281									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-582-450-1									
Query Match 100.0%; Score 1287; DB 4; Length 281;									
Best Local Similarity 100.0%; Pred. No. 2.9e-125;									
Matches	243;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE	60						
Db	39	TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE	98						
Qy	61	TISTVQEKQONISPLVREGRQPQVAHIITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	120						
Db	99	TISTVQEKQONISPLVREGRQPQVAHIITGTRGRSNTLSSPNSKNEKALGRKINS							

RESULT 12									
US-09-934-465-1									
; Sequence 1, Application US/09934465									
; Patent No. 6746668									
; GENERAL INFORMATION:									
; APPLICANT: Ashkenazi, Avi J.									
; TITLE OF INVENTION: APO-2 LIGAND									
; FILE REFERENCE: 11669.22US03									
; CURRENT APPLICATION NUMBER: US/09/934,465									
; CURRENT FILING DATE: 2001-08-21									
; PRIOR APPLICATION NUMBER: 08/584,031									
; PRIOR FILING DATE: 1996-01-09									
; NUMBER OF SEQ ID NOS: 17									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 1									
; LENGTH: 281									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-934-465-1									
Query Match 100.0%; Score 1287; DB 4; Length 281;									
Best Local Similarity 100.0%; Pred. No. 2.9e-125;									
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVKWQLRQLVRKMILRTSEE	60						
DB	39	TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVKWQLRQLVRKMILRTSEE	98						
QY	61	TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	120						
DB	99	TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	158						
QY	121	SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYD	180						
DB	159	SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYD	218						
QY	181	PILLMKSARNCSWSDAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	240						
DB	219	PILLMKSARNCSWSDAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	278						
QY	241	LVG 243							
DB	279	LVG 281							
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US-10-011-125A-4									
; Sequence 4, Application US/10011125A									
; Patent No. 6828121									
; GENERAL INFORMATION:									
; APPLICANT: Chen, Christina Yu-Ching									
; TITLE OF INVENTION: BACTERIAL HOST STRAINS									
; FILE REFERENCE: P1804R1									
; CURRENT APPLICATION NUMBER: US/10/011,125A									
; CURRENT FILING DATE: 2001-12-07									
; PRIOR APPLICATION NUMBER: US 60/256,162									
; PRIOR FILING DATE: 2000-12-14									
; NUMBER OF SEQ ID NOS: 12									
; SEQ ID NO 4									
; LENGTH: 281									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-011-125A-4									
Query Match 100.0%; Score 1287; DB 4; Length 281;									
Best Local Similarity 100.0%; Pred. No. 2.9e-125;									
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	39	TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVKWQLRQLVRKMILRTSEE	98						
QY	61	TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	120						
RESULT 14									
PCT-US96-10895-2									
; Sequence 2, Application PC/TUS9610895									
; GENERAL INFORMATION:									
; APPLICANT: Immunex Corporation.									
; TITLE OF INVENTION: Cytokine That Induces Apoptosis									
; NUMBER OF SEQUENCES: 9									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation									
; STREET: 51 University Street									
; CITY: Seattle									
; STATE: WA									
; COUNTRY: USA									
; ZIP: 98101									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
; COMPUTER: Apple Macintosh									
; OPERATING SYSTEM: Apple 7.5.2									
; SOFTWARE: Microsoft Word, Version 6.0.1									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: PCT/US96/10895									
; FILING DATE: 25-JUN-1996									
; CLASSIFICATION:									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER: US 08/496,632									
; FILING DATE: 29-JUN-1995									
; CLASSIFICATION:									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER: US 08/548,368									
; FILING DATE: 01-NOV-1995									
; CLASSIFICATION:									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Anderson, Kathryn A.									
; REGISTRATION NUMBER: 32,172									
; REFERENCE/DOCKET NUMBER: 2835-WO									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: (206) 587-0430									
; TELEFAX: (206) 233-0644									
; TELEX: 756822									
; INFORMATION FOR SEQ ID NO: 2:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 281 amino acids									
; TYPE: amino acid									
; TOPOLOGY: linear									
; MOLECULE TYPE: protein									
PCT-US96-10895-2									
Query Match 100.0%; Score 1287; DB 5; Length 281;									
Best Local Similarity 100.0%; Pred. No. 2.9e-125;									
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVKWQLRQLVRKMILRTSEE	60						
DB	39	TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVKWQLRQLVRKMILRTSEE	98						
QY	61	TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	120						

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Db      99 TISTVQEKQONISPLVRGPQVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSR 158
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Db      159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYPD 218
Qy      181 PILLMKSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db      219 PILLMKSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy      241 LVG 243
Db      279 LVG 281
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RESULT 15

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US-09-569-611C-30
; Sequence 30, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-30
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Query Match 81.4%; Score 1047; DB 4; Length 271;

Best Local Similarity 83.1%; Pred. No. 2.2e-100;

Matches 202; Conservative 2; Mismatches 5; Indels 34; Gaps 2;

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Qy      1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVQWLRLQVRLKMLRTSEE 60
Db      63 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVQWLRLQVRLK----- 114
Qy      61 TISTVQEKQONISPLVRGPQVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db      115 -----KSNKIFLPLVRGPQVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSR 168
Qy      121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYPD 180
Db      169 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYPD 228
Qy      181 PILLMKSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db      229 PILLMKSARNCSKDAEYGLYSIYOG-----IDMDHEASFFGAF 268
Qy      241 LVG 243
Db      269 LVG 271
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Search completed: June 22, 2005, 06:02:16

Job time : 28.8244 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2005, 06:19:02 ; Search time 40 Seconds
(without alignments)
675.923 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MAMMEVGGPSLGTCVLIV.....NEHLMDHRAFFGAPLVG 281

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

1: PIR.79.*

2: PIR.2.*

3: PIR.3.*

4: PIR.4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	2.8	643	2 G75599	probable drug tran
2	8	2.8	950	2 T09076	hypothetical prote
3	7	2.5	51	2 S63590	insulin - duckbill
4	7	2.5	93	2 F84175	hypothetical prote
5	7	2.5	96	2 F80423	H4 protein - Toxop
6	7	2.5	107	2 C90304	hypothetical prote
7	7	2.5	155	2 G72548	hypothetical prote
8	7	2.5	240	2 A39016	T-cell surface gly
9	7	2.5	247	2 D90053	hypothetical prote
10	7	2.5	251	2 T40807	hypothetical prote
11	7	2.5	263	2 T38003	hypothetical ser-t
12	7	2.5	327	2 H82736	hypothetical prote
13	7	2.5	329	2 D71887	ADPglyceromanno-he
14	7	2.5	354	2 G71465	hypothetical prote
15	7	2.5	354	2 A81728	conserved hypotet
16	7	2.5	401	2 C82660	conserved hypotet
17	7	2.5	404	2 G90210	hypothetical prote
18	7	2.5	420	2 S53916	SUN4 protein precu
19	7	2.5	424	2 H84806	hypothetical prote
20	7	2.5	427	2 G71272	iron-sulfur cofact
21	7	2.5	428	2 B84192	zinc metalloprotei
22	7	2.5	429	2 B72109	GMP synthase CP059
23	7	2.5	429	2 C86512	GMP synthase [limp
24	7	2.5	442	2 AF2539	manganese transpor
25	7	2.5	475	2 T39359	probable udp-n-ace
26	7	2.5	511	2 T19496	hypothetical prote
27	7	2.5	554	2 A47503	epoxide hydrolase
28	7	2.5	565	2 C82280	sensor kinase cita
29	7	2.5	710	2 T22360	hypothetical prote

30	7	2.5	801	2 AE3032	conserved hypotet
31	7	2.5	801	2 G98253	hypothetical prote
32	7	2.5	809	2 T20430	hypothetical prote
33	7	2.5	913	2 D90183	ATP-dependent heli
34	7	2.5	926	2 T15683	hypothetical prote
35	7	2.5	979	2 JH0109	glycoprotein 14 pr
36	7	2.5	982	2 E88465	protein B0244.6 [i
37	7	2.5	1014	2 T36031	exonuclease ABC c
38	7	2.5	1377	2 T19214	UDP-glucose-glycop
39	7	2.5	1414	2 T33236	hypothetical prote
40	7	2.5	1847	2 E64477	replication factor
41	7	2.5	1891	2 T43262	calcium channel al
42	7	2.5	1975	2 B81192	hemagglutinin/hemo
43	7	2.5	1995	2 G81044	hemagglutinin/hemo
44	7	2.5	2015	2 B81989	hypothetical prote
45	7	2.5	3434	1 GNVVMV	genome polyprotein
46	6	2.1	47	2 T04365	ethylene responsiv
47	6	2.1	48	2 S78202	H+-transporting tw
48	6	2.1	55	2 AP2105	hypothetical prote
49	6	2.1	56	2 C60157	hypothetical prote
50	6	2.1	62	2 C97621	hypothetical prote
51	6	2.1	64	2 AG0025	probable bacteriof
52	6	2.1	65	2 AC0774	hypothetical prote
53	6	2.1	85	2 C91249	hypothetical prote
54	6	2.1	89	2 S78744	protein YDR163w-a
55	6	2.1	96	2 B82311	conserved hypotet
56	6	2.1	96	2 AE3205	transposase tnp [i
57	6	2.1	98	2 G91248	hypothetical prote
58	6	2.1	102	2 C95337	probable cytochrom
59	6	2.1	104	2 E59832	conserved hypotet
60	6	2.1	105	2 B86818	hypothetical prote
61	6	2.1	107	2 S09964	ig kappa chain V-J
62	6	2.1	107	2 A44887	glucose transporte
63	6	2.1	109	2 F84012	hypothetical prote
64	6	2.1	112	2 AC2887	conserved hypotet
65	6	2.1	112	2 H97662	hypothetical prote
66	6	2.1	115	2 B25924	ig kappa chain pre
67	6	2.1	116	2 C83166	probable chaperone
68	6	2.1	117	2 F97174	hypothetical prote
69	6	2.1	119	2 JQ2032	lambda 208 protei
70	6	2.1	122	2 D89803	conserved hypotet
71	6	2.1	128	2 AH0043	probable lipoprote
72	6	2.1	130	2 D64559	hypothetical prote
73	6	2.1	132	2 F86829	ribose ABC transpo
74	6	2.1	132	2 F70650	hypothetical prote
75	6	2.1	134	2 AC0855	probable regulator
76	6	2.1	135	2 B91078	transcription regu
77	6	2.1	135	2 T44999	hypothetical prote
78	6	2.1	137	2 S74888	hypothetical prote
79	6	2.1	137	2 D86944	conserved hypotet
80	6	2.1	137	2 T30095	hypothetical prote
81	6	2.1	137	2 F89954	conserved hypotet
82	6	2.1	143	1 WMB56H	transcription regu
83	6	2.1	143	2 T43976	transactivator lim
84	6	2.1	143	2 B71372	conserved hypotet
85	6	2.1	145	2 AC0053	DNA-directed DNA p
86	6	2.1	146	2 C85923	probable regulator
87	6	2.1	149	2 H70581	hypothetical prote
88	6	2.1	151	2 A75297	hypothetical prote
89	6	2.1	152	2 B64485	hypothetical prote
90	6	2.1	152	2 T43088	traj protein homol
91	6	2.1	154	2 F90546	deoxycytidylate de
92	6	2.1	157	2 A84402	hypothetical prote
93	6	2.1	161	2 H87183	integral membrane
94	6	2.1	162	2 T50253	Vacuolar ATP synth
95	6	2.1	165	2 S62563	adaptin complex sm
96	6	2.1	166	2 A75426	hypothetical prote
97	6	2.1	167	2 G95335	hypothetical prote
98	6	2.1	169	2 D72765	hypothetical prote
99	6	2.1	169	2 T31484	hypothetical prote
100	6	2.1	170	2 T48974	hypothetical prote

ALIGNMENTS

RESULT 1

G75599
probable drug transport protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: G75599
R:White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: G75599

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-643 <WHI>

A:Cross-references: UNIPROT:Q9RZ93; GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF1225

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRA0061

A:Map position: 2

Query Match 2.8%; Score 8; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLIVIFTV 24

|||||

DB 231 VLIVIFTV 238

RESULT 2

T09076
hypothetical protein CGI (strain HB3) - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T09076
R:Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellem, T.E.
Cell 91, 593-603, 1997

A:Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant

A:Reference number: Z16556; MUID:98054002; PMID:9393853

A:Accession: T09076

A>Status: translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-950 <SUX>

A:Cross-references: UNIPROT:O15788; EMBL:AF030690; NID:g2642510; PIDN:AAC47851.1; PID:g2

C:Genetics:

A:Gene: cgl

Query Match 2.8%; Score 8; DB 2; Length 950;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140

|||||

DB 361 SNTLSSPN 368

RESULT 3

S63590
insulin - duckbill platypus
C:Species: Ornithorhynchus anatinus (duckbill platypus)
C:Date: 19-Mar-1997 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: S63591; S63590
R:Nourse, A.; Treacy, G.B.; Shaw, D.C.; Jeffrey, P.D.
Biol. Chem. Hoppe-Seyler 377, 147-153, 1996

A:Title: Platypus insulin: indications from the amino acid sequence of significant differ

A:Reference number: S63590; MUID:97021710; PMID:8868070

A:Accession: S63591

A:Molecule type: protein

A:Residues: 1-30 <NOU2>
A:Cross-references: UNIPROT:Q9TQY7
A:Accession: S63590
A:Molecule type: protein
A:Residues: 31-51 <NOUI>
C:Superfamily: insulin
C:Key words: hormone; pancreas
F:1-30/31-51/Product: insulin #status experimental <MAT>
F:1-30/Domain: insulin chain B #status experimental <BCH>
F:31-51/Domain: insulin chain A #status experimental <ACH>
F:7-37/19-50/36-41/Disulfide bonds: #status predicted

Query Match 2.5%; Score 7; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 EKGFFYYI 184

|||||

DB 21 EKGFFYYI 27

RESULT 4

F84175
hypothetical protein Vng0151c [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: F84175
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lia

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: F84175

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-93 <STO>

A:Cross-references: UNIPROT:Q9HSN3; GB:AE004437; NID:g10579798; PIDN:AAG18770.1; GSPDB:G

C:Genetics:

A:Gene: VNG0151C

Query Match 2.5%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 FVSVTNE 263

|||||

DB 13 FVSVTNE 19

RESULT 5

PS0423
H4 protein - Toxoplasma gondii (fragment)
N:Alternate names: diagnostic antigen H4
C:Species: Toxoplasma gondii
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C:Accession: PS0423
R:Johnson, A.M.; Iilana, S.
Gene 99, 127-132, 1991

A:Title: Cloning of Toxoplasma gondii gene fragments encoding diagnostic antigens.

A:Reference number: PS0423; MUID:91216437; PMID:2022319

A:Accession: PS0423

A:Molecule type: mRNA

A:Residues: 1-96 <JOH>

A:Cross-references: UNIPROT:Q27001; GB:M57302; NID:g161914; PID:g161915

C:Genetics:

A:Gene: H4

Query Match 2.5%; Score 7; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FOREIKE 198
|||||
Db 2 FOREIKE 8

RESULT 6

C90304
hypothetical protein SS01462 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: C90304
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.
arrett, R.A.; Ragan, M.A.; Senen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: C90304
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <KUR>
A;Cross-references: UNIPROT:Q97Y77; GB:AE006641; NID:gl3814690; PIDN:AAK41690.1; GSPDB:G
C;Genetics:
A;Gene: SS01462

Query Match 2.5%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 FFGAFLV 280
|||||
Db 46 FFGAFLV 52

RESULT 7

G72548
hypothetical protein APE1675 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72548
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72548
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-155 <KAW>
A;Cross-references: UNIPROT:Q9YBC2; DDBJ:AP000062; NID:gs105244; PIDN:BAAB0676.1; PID:dl
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1675

Query Match 2.5%; Score 7; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 TLSSPNS 141
|||||
Db 88 TLSSPNS 94

RESULT 8

A39016
T-cell surface glycoprotein CD7 precursor - human
N;Alternate names: T-cell leukemia antigen
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C;Accession: A39016; S03520
R;Schamborg, L.E.; Fleener, D.E.; Kurtzberg, J.; Haynes, B.F.; Kaufman, R.E.
Proc. Natl. Acad. Sci. U.S.A. 88, 603-607, 1991
A;Title: Isolation and characterization of the genomic human CD7 gene: structural simila

A;Reference number: A39016; MUID:91110576; PMID:1703303

A;Accession: A39016

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-240 <SCH>

A;Cross-references: UNIPROT:P09564; GB:M37271; NID:gl80163; PIDN:AAA51953.1; PID:gl80164

R;Aruffo, A.; Seed, B.

EMBO J. 6, 3313-3316, 1987

A;Title: Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS cell expr

A;Reference number: S03520; MUID:88111517; PMID:3501369

A;Accession: S03520

A;Molecule type: mRNA

A;Residues: 1-240 <ARU>

A;Cross-references: EMBL:X06180; NID:g29819; PIDN:CAA29546.1; PID:g732757

C;Genetics:

A;Gene: GDB:CD7

A;Cross-references: GDB:119770; OMIM:186820

A;Map position: 17q25.2-17q25.3

A;Introns: 28/1

C;Keywords: glycoprotein; membrane protein; surface antigen; tandem repeat

F;1-25/Domain: signal sequence #status predicted <SIG>

F;26-240/Product: T-cell surface glycoprotein CD7 #status predicted <MAT>

F;145-180/Region: 9-residue repeats (X-P-P-X-A-S-A-L-P)

Query Match 2.5%; Score 7; DB 2; Length 240;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 NTLSSPN 140
|||||
Db 231 NTLSSPN 237

RESULT 9

D90053
hypothetical protein sarH2 [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: D90053

R;Kuroda, M.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaifo, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: D90053

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-247 <KUR>

A;Cross-references: UNIPROT:Q99RD5; GB:BA000018; PID:gl3702449; PIDN:BAAB43590.1; GSPDB:G

A;Experimental source: strain N315

C;Genetics:

A;Gene: sarH2

Query Match 2.5%; Score 7; DB 2; Length 247;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
|||||
Db 91 RIFVSVT 97

RESULT 10

T40807

hypothetical protein SPBP87.13 - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T40807

R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, October 1998

A;Reference number: Z21949

A;Accession: T40807

A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-251 <REC>
A:Cross-references: UNIPROT:O94262; EMBL:AL032684; PIDN:CAA21798.1; GSPDB:GN00067; SPDB:
A:Experimental source: strain 972h; clone pl p8B7
C:Genetics:
A:Gene: SPDB:SPBP87.13
A:Map position: 2
A:Introns: 54/1
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBP87.13

Query Match 2.5%; Score 7; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DPNDEES 72
|||||
DB 73 DPNDEES 79

RESULT 11
T38003
hypothetical ser-thr rich protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Nov-2000
C:Accession: T38003
R:Oliver, K.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1997
A:Reference number: Z21760
A:Accession: T38003
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-263 <OLI>
A:Cross-references: EMBL:Z97209; PIDN:CAB10128.1; GSPDB:GN00066; SPDB:SPAC19G12.16C
A:Experimental source: strain 972h; cosmid c19G12
C:Genetics:
A:Gene: SPAC23A1.01c; SPDB:SPAC19G12.16C
A:Map position: 1
C:Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase

Query Match 2.5%; Score 7; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 EETISTV 103
|||||
DB 177 EETISTV 183

RESULT 12
H82736
hypothetical protein XP0992 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82736
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82736
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <SIM>
A:Cross-references: UNIPROT:QPPENG; GB:AE003937; GB:AE003849; NID:g9105920; PIDN:AAF8380
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.;
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0992

Query Match 2.5%; Score 7; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117
|||||
DB 164 SPLVRER 170

RESULT 13
D71887
ADPglyceromanno-heptose 6-epimerase (EC 5.1.3.20) gmhd homolog [similarity] - Helicobacte
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: D71887
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: D71887
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-329 <ARN>
A:Cross-references: UNIPROT:Q9ZKY9; GB:AE001509; GB:AE001439; NID:g4155350; PIDN:AAD0636;
A:Experimental source: strain J99
C:Genetics:
A:Gene: gmhd
C:Superfamily: ADPglyceromanno-heptose 6-epimerase; UDPglucose 4-epimerase homology
C:Keywords: isomerase

Query Match 2.5%; Score 7; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RSNTLSS 138
|||||
DB 46 RSNTLSS 52

RESULT 14
G71465
hypothetical protein CT839 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: G71465
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tract
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: G71465
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <ARN>
A:Cross-references: UNIPROT:O84846; GB:AE001356; GB:AE001273; NID:g3329299; PIDN:AAC6843;
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: CT839

Query Match 2.5%; Score 7; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
 Db 150 KENDRIF 156

RESULT 15

A81728
 conserved hypothetical protein TC0227 [imported] - Chlamydia muridarum (strain Nigg)
 C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: A81728
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Ginn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: A81728
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-354 <TET>
 A:Cross-references: UNIPROT:Q9PL80; GB:AE002289; GB:AE002160; NID:97190254; PIDN:AAF3909
 A:Experimental source: strain Nigg (MoPn)
 C:Genetics:
 A:Gene: TC0227

Query Match 2.5%; Score 7; DB 2; Length 354;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
 Db 150 KENDRIF 156

RESULT 16

C82660
 conserved hypothetical protein XF1611 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: C82660
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing 405, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: C82660
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-401 <SIM>
 A:Cross-references: UNIPROT:Q9PC23; GB:AE003988; GB:AE003849; NID:99106653; PIDN:AAF8442
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak M.; Teuhako, M.H.; Vallada, H.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva M.; Reference number: A59328
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF1611
 C:Superfamily: Escherichia coli hypothetical 48K protein (glnA-fdhE region)

Query Match 2.5%; Score 7; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 DAEYGLY 240
 Db 157 DAEYGLY 163

RESULT 17

G90210
 hypothetical protein purF-2 [imported] - Sulfolobus solfataricus
 C:Species: Sulfolobus solfataricus
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C:Accession: G90210
 R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awavez, M.J.; Chan-y jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.
 A:Reference number: A99139
 A:Accession: G90210
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-404 <KUR>
 A:Cross-references: UNIPROT:Q9UX27; GB:AE006641; NID:gl3813800; PIDN:AAK40942.1; GSPDB:CG
 C:Genetics:
 A:Gene: purF-2

Query Match 2.5%; Score 7; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 YKSGGIA 55
 Db 35 YKSGGIA 41

RESULT 18

S53916
 SUN4 protein precursor - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein N2411; protein YNL066w; protein YNL1612
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C:Accession: S53916; S58712; S62994; S62998; S63945
 R:Poehlmann, R.; Philippsen, P.
 submitted to the EMBL Data Library, April 1995
 A:Reference number: S53896
 A:Accession: S53916
 A:Molecule type: DNA
 A:Residues: 1-420 <POE>
 A:Cross-references: UNIPROT:P53616; EMBL:X86470; NID:g791101; PID:g791122
 R:Bergez, P.; Doignon, F.; Crouzet, M.
 Yeast 11, 967-974, 1995
 A:Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV f
 A:Reference number: S58711; MUID:96021608; PMID:8533472
 A:Accession: S58712
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-420 <BER>
 A:Cross-references: EMBL:U12141; NID:gl314216; PIDN:AAA99645.1; PID:g994821
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
 R:Bergez, P.; Doignon, F.; Crouzet, M.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62975
 A:Accession: S62994
 A:Molecule type: DNA
 A:Residues: 1-420 <BEF>
 A:Cross-references: EMBL:Z71342; NID:gl301944; PID:gl301945; MIPS:YNL066w
 A:Experimental source: strain S288C
 R:Poehlmann, R.; Philippsen, P.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62997
 A:Accession: S62998
 A:Molecule type: DNA
 A:Residues: 1-420 <POW>

A;Cross-references: EMBL:Z71342; NID:g1301944; PID:g1301945; MIPS:YNL066w
 A;Experimental source: strain S288C
 R;Poehlmann, R.; Philippsen, P.
 Yeast 12, 391-402, 1996
 A;Title: Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV reveals 12
 A;Reference number: S63925; MUID:96267764; PMID:8701611
 A;Accession: S63945
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-420 <POF>
 A;Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60196.1; PID:g791122
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
 C;Genetics:
 A;Gene: SGD:SUN4
 A;Cross-references: SGD:S0005010; MIPS:YNL066w
 A;Map position: 14L
 A;Genome: nuclear
 C;Superfamily: Saccharomyces NCA3 protein
 C;Keywords: mitochondrion
 F;1-46/Domain: transit peptide (mitochondrion) #status predicted <TNP>
 F;46-420/Product: SUN4 protein #status predicted <MAT>

Query Match 2.5%; Score 7; DB 2; Length 420;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 VAVTVYV 37
 |||||
 Db 47 VAVTVYV 53

RESULT 19
 H84806
 hypothetical protein At2g38590 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: H84806
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 408, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: H84806
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-424 <STO>
 A;Cross-references: UNIPROT:Q92V11; GB:AE002093; NID:g3786013; PIDN:AAC67359.1; GSPDB:GN
 C;Genetics:
 A;Gene: At2g38590
 A;Map position: 2
 C;Superfamily: Arabidopsis thaliana hypothetical protein T1F15.9

Query Match 2.5%; Score 7; DB 2; Length 424;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 CFLKEDD 62
 |||||
 Db 122 CFLKEDD 128

RESULT 20
 G71272
 iron-sulfur cofactor synthesis protein nifs2 TP0863 [similarity] - syphilis spirochete
 N;Contains: L-cysteine sulfurtransferase (EC 2.8.1.-)
 C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C;Accession: G71272
 R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khaliq, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 . Science 281, 375-388, 1998

A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A;Reference number: A71250; MUID:98332770; PMID:9665876
 A;Accession: G71272
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-427 <COL>
 A;Cross-references: UNIPROT:O83835; GB:AE001256; GB:AE000520; NID:g3323171; PIDN:AAC6582
 A;Experimental source: strain Nichols
 C;Genetics:
 A;Gene: TP0863
 C;Superfamily: nitrogen fixation protein nifs
 C;Keywords: phosphoprotein; pyridoxal phosphate; sulfurtransferase
 F;232/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
 F;374/Active site: Cys (cysteine persulfide intermediate) #status predicted

Query Match 2.5%; Score 7; DB 2; Length 427;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TGTGRGS 133
 |||||
 Db 166 TGTGRGS 172

RESULT 21
 E84192
 zinc metalloproteinase homolog [imported] - Halobacterium sp. NRC-1
 C;Species: Halobacterium sp. NRC-1
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: E84192
 R;Leithausner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabor
 i; Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; MUID:20504483; PMID:11016950
 A;Accession: E84192
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-428 <STO>
 A;Cross-references: UNIPROT:Q9HSA2; GB:AE004437; NID:g10579955; PIDN:AGI8905.1; GSPDB:GN
 C;Genetics:
 A;Gene: caax

Query Match 2.5%; Score 7; DB 2; Length 428;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 SSRSQHS 162
 |||||
 Db 237 SSRSQHS 243

RESULT 22
 B72109
 GMP synthase CP0599 [imported] - Chlamydomophila pneumoniae (strains CWL029 and AR39)
 C;Species: Chlamydomophila pneumoniae; Chlamydia pneumoniae
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: B72109; E81558
 R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
 Nature Genet. 21, 385-389, 1999
 A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A;Reference number: A72000; MUID:99206606; PMID:10192388
 A;Accession: B72109
 A;Molecule type: DNA
 A;Residues: 1-429 <ARN>
 A;Cross-references: UNIPROT:Q9Z913; GB:AE001604; GB:AE001363; NID:g4376438; PIDN:AAD1823
 A;Experimental source: strain CWL029
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I
 . C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: AB1500; MUID:20150255; PMID:10684935

A:Accession: E81558

A:Molecule type: DNA

A:Residues: 1-429 <REA>

A:Cross-references: GB:AE002218; GB:AE002161; NID:g7189509; PIDN:AAF38415.1; PID:g718951

A:Experimental source: strain AR39, HL cells

C:Genetics:

A:Gene: guaA; CP0599

C:Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology

F;11-194/Domain: trpG homology <TRG>

Query Match 2.5%; Score 7; DB 2; Length 429;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSRGH 161

|||||

Db 248 ESSRSRGH 254

RESULT 23

C86512

GMP synthase [imported] - Chlamydophila pneumoniae (strain J138)

C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: C86512

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: C86512

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-429 <STO>

A:Cross-references: UNIPROT:Q92913; GB:BA000008; NID:g8978544; PIDN:BAA98381.1; GSPDB:GN

A:Experimental source: strain J138

C:Genetics:

A:Gene: guaA

C:Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology

Query Match 2.5%; Score 7; DB 2; Length 429;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSRGH 161

|||||

Db 248 ESSRSRGH 254

RESULT 24

AF2539

manganese transport protein all7601 [imported] - Nostoc sp. (strain PCC 7120) plasmid pC

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AF2539

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AF2539

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-442 <KUR>

A:Cross-references: UNIPROT:Q92S80; GB:AP003602; PIDN:BAF77244.1; PID:g17134686; GSPDB:G

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all7601

A:Genome: plasmid

C:Superfamily: natural resistance-associated macrophage protein 1

Query Match 2.5%; Score 7; DB 2; Length 442;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 LQSLCV 31

|||||

Db 76 LQSLCV 82

RESULT 25

T39359

probable udp-n-acetylglucosamine pyrophosphorylase - fission yeast (Schizosaccharomyces

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T39359

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.

submitted to the EMBL Data Library, March 1999

A:Reference number: Z21848

A:Accession: T39359

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-475 <WOO>

A:Cross-references: UNIPROT:O94617; EMBL:AL035675; PIDN:CAB38688.1; GSPDB:GN00067; SPDB:SF

A:Experimental source: strain 972h-; cosmid c1289

C:Genetics:

A:Gene: SPDB:SPBC1289.08

A:Map position: 2

Query Match 2.5%; Score 7; DB 2; Length 475;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETIS 101

|||||

Db 168 TSEETIS 174

RESULT 26

T19496

hypothetical protein C27A7.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000

C:Accession: T19496

R:Harris, B.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19132

A:Accession: T19496

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-511 <WIL>

A:Cross-references: EMBL:Z81041; PIDN:CAB02786.1; GSPDB:GN00023; CESP:C27A7.2

A:Experimental source: clone C27A7

C:Genetics:

A:Gene: CESP:C27A7.2

A:Map position: 5

A:Introns: 44/3; 87/2; 130/2; 164/3; 203/2; 273/3; 325/1; 369/2

C:Superfamily: Caenorhabditis elegans hypothetical protein F07G11.3

Query Match 2.5%; Score 7; DB 2; Length 511;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 YKSGIA 55

|||||

Db 120 YKSGIA 126

RESULT 27

A47503

epoxide hydrolase (EC 3.3.2.3), cytosolic - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A47503; S17104; S19319

R:Knehr, M.; Thomas, H.; Arand, M.; Gebel, T.; Zeller, H.D.; Oesch, F.

J. Biol. Chem. 268, 17623-17627, 1993
 A>Title: Isolation and characterization of a cDNA encoding rat liver cytosolic epoxide hydrolase
 A:Reference number: A47503; MUID:93352557; PMID:8349641
 A:Accession: A47503
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-554 <RNE>
 A:Cross-references: UNIPROT:P80299; GB:X65083; NID:g402631; PIDN:CAA46211.1; PID:g402632
 A:Experimental source: liver
 A>Note: sequence extracted from NCBI backbone (NCBIN:136329, NCEIP:136330)
 R:Arand, M.; Knehr, M.; Thomas, H.; Zeller, H.D.; Oesch, F.
 submitted to the EMBL Data Library, September 1991
 A:Description: The unusual bicompartimental distribution of cytosolic epoxide hydrolase
 A:Reference number: S17104
 A:Accession: S17104
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 450-554 <ARA>
 A:Cross-references: EMBL:X60328; NID:g55929; PIDN:CAA42898.1; PID:g55930
 R:Arand, M.; Knehr, M.; Thomas, H.; Zeller, H.D.; Oesch, F.
 FEBS Lett. 294, 19-22, 1991
 A>Title: An impaired peroxisomal targeting sequence leading to an unusual bicompartimental distribution of cytosolic epoxide hydrolase
 A:Reference number: S19319; MUID:92077134; PMID:1743286
 A:Accession: S19319
 A:Molecule type: mRNA
 A:Residues: 448-554 <AR2>
 A:Keywords: cytosol; ether hydrolase

Query Match 2.5%; Score 7; DB 2; Length 554;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 KALGRKI 151
 Db 477 KALGRKI 483

RESULT 28
 C82280
 sensor kinase cita VC0791 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: C82280
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; McDonald, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: C82280
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-565 <HEI>
 A:Cross-references: UNIPROT:Q9KTU6; GB:AE004164; GB:AE003852; NID:g9655232; PIDN:AAF9395
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC0791
 A:Map position: 1
 C:Superfamily: two-component sensor histidine kinase; sensor histidine kinase homology

Query Match 2.5%; Score 7; DB 2; Length 565;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 VIPTVLL 26
 Db 185 VIPTVLL 191

RESULT 29
 T22360
 hypothetical protein F47G4.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 A:Accession: T22360
 R:White, S.
 submitted to the EMBL Data Library, September 1997
 A:Reference number: Z19553
 A:Accession: T22360
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-710 <WIL>
 A:Cross-references: UNIPROT:Q9XTS0; EMBL:Z99171; PIDN:CAB16314.1; GSPDB:GN00019; CESP:F4;
 A:Experimental source: clone F47G4
 C:Genetics:
 A:Gene: CESP:F47G4.2
 A:Map position: 1
 A:Introns: 20/1; 131/3; 220/2; 273/1; 380/2; 577/2

Query Match 2.5%; Score 7; DB 2; Length 710;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 ILRTSEE 98
 Db 647 ILRTSEE 653

RESULT 30
 AE3032
 conserved hypothetical protein Atu3866 [imported] - Agrobacterium tumefaciens (strain C58)
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AE3032
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClelland, Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AE3032
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-801 <KUR>
 A:Cross-references: UNIPROT:Q8U963; GB:AE008689; PIDN:AAL44675.1; PID:g17742302; GSPDB:G1
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu3866
 A:Map position: linear chromosome

Query Match 2.5%; Score 7; DB 2; Length 801;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ASFFGAF 278
 Db 216 ASFFGAF 222

RESULT 31
 G98253
 hypothetical protein AGR_L1958 [imported] - Agrobacterium tumefaciens (strain C58, Cere)
 C:Species: Agrobacterium tumefaciens
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: G98253
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: G98253
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-801 <KUR>

A;Cross-references: UNIPROT:Q8U963; GB:AE007870; PIDN:AAK9553.1; PID:gl3159435; GSPDB:G
 C;Genetics:
 A;Gene: AGK_L_1958
 A;Map position: linear chromosome

Query Match 2.5%; Score 7; DB 2; Length 801;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ASFFGAF 278
 |||||
 Db 216 ASFFGAF 222

RESULT 32
 T20430
 hypothetical protein E03A3.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T20430

R;Gardner, A.
 submitted to the EMBL Data Library, October 1994
 A;Reference number: Z19274
 A;Accession: T20430
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-809 <WIL>
 A;Cross-references: UNIPROT:Q19046; EMBL:Z38112; PIDN:CAA86232.1; GSPDB:GNO0021; CESP:EQ
 A;Experimental source: clone E03A3
 C;Genetics:
 A;Gene: CESP:E03A3.2
 A;Map position: 3
 A;Introns: 49/3; 144/1; 319/2; 376/3; 484/2; 540/3; 573/2; 612/3; 720/3; 776/3

Query Match 2.5%; Score 7; DB 2; Length 809;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 EYGLYSI 242
 |||||
 Db 756 EYGLYSI 762

RESULT 33
 D90183
 ATP-dependent helicase [imported] - Sulfolobus solfataricus
 C;Species: Sulfolobus solfataricus
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: D90183

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
 arrett, R.A.; Ragan, M.A.; SENSEN, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A;Description: Sulfolobus solfataricus complete genome.
 A;Reference number: A99139
 A;Accession: D90183
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-913 <KUR>
 A;Cross-references: UNIPROT:Q980C0; GB:AE006641; NID:gl3813545; PIDN:AAK40723.1; GSPDB:G
 C;Genetics:
 A;Gene: S800394

Query Match 2.5%; Score 7; DB 2; Length 913;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 ENDRIFV 258
 |||||
 Db 517 ENDRIFV 523

RESULT 34

T15683
 hypothetical protein C28C12.10 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T15683

R;Miller, N.
 submitted to the EMBL Data Library, November 1995
 A;Description: The sequence of C. elegans cosmid C28C12.
 A;Reference number: Z18387
 A;Accession: T15683
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-926 <WIL>
 A;Cross-references: UNIPROT:Q18284; EMBL:U40797; NID:gl065916; PID:gl065927; PIDN:AA8375
 A;Experimental source: strain Bristol N2; clone C28C12
 C;Genetics:
 A;Gene: CESP:C28C12.10
 A;Map position: 4
 A;Introns: 18/3; 98/2; 173/2; 206/3; 298/3; 405/3; 488/3; 727/3; 761/1; 828/2

Query Match 2.5%; Score 7; DB 2; Length 926;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 DEESMNS 75
 |||||
 Db 122 DEESMNS 128

RESULT 35
 JH0109
 glycoprotein 14 precursor - equine herpesvirus 1
 C;Species: equine herpesvirus 1
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C;Accession: JH0109

R;Guo, P.
 Gene 87, 249-255, 1990
 A;Title: Characterization of the gene and an antigenic determinant of equine herpesvirus
 A;Reference number: JH0109; MUID:90236317; PMID:1692002
 A;Accession: JH0109
 A;Molecule type: DNA
 A;Residues: 1-979 <GUO>
 A;Cross-references: UNIPROT:P25218; GB:M34861; NID:g330900; PIDN:AAA46086.1; PID:g330901
 A;Note: Glycoprotein 14 is homologous to corresponding glycoprotein of pseudorabies, bo
 C;Genetics:
 A;Gene: gp14
 C;Superfamily: herpesvirus glycoprotein B
 C;Keywords: glycoprotein; transmembrane protein
 F;1-86/Domain: signal sequence #status predicted <SIG>
 F;87-979/Product: glycoprotein 14 #status predicted <MAT>
 F;831-871/Region: hydrophobic
 F;165,275,380,423,457,514,560,727,749,951,970/Binding site: carbohydrate (Asn) (covalent)

Query Match 2.5%; Score 7; DB 2; Length 979;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 SGIACFL 58
 |||||
 Db 839 SGIACFL 845

RESULT 36
 E88465
 protein B0244.6 [imported] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C;Accession: E88465

R;anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
 A;Reference number: A75000; MUID:99069613; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/

A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: E88465
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-982 <STO>
 A:Cross-references: UNIPROT:Q09965; GB:chr_III; PIDN:AAA68379.1; PID:9861359; GSPDB:GN000019;
 C:Genetics:
 A:Gene: B0244.6
 A:Map position: 3

Query Match 2.5%; Score 7; DB 2; Length 982;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RSNLTSS 138
 DB 461 RSNLTSS 467
 |||||

RESULT 37
 T36031
 excinuclease ABC chain A SCC54.18c [similarity] - Streptomyces coelicolor
 N:Contains: excision endonuclease ABC (EC 3.1.1.-) chain A
 C:Species: Streptomyces coelicolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T36031
 R:Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, March 1999
 A:Reference number: T21581
 A:Accession: T36031
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1014 <SES>
 A:Cross-references: UNIPROT:Q92507; EMBL:AL035591; PIDN:CAB38148.1; GSPDB:GN000070; SCOE
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: uvrA; SCOE:SCC54.18c
 C:Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
 C:Keywords: ATP; DNA binding; DNA repair; hydrolase; nucleotide binding; P-loop
 F:32-39/Region: nucleotide-binding motif A (P-loop)
 F:645-652/Region: nucleotide-binding motif A (P-loop)

Query Match 2.5%; Score 7; DB 2; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117
 DB 153 SPLVRER 159
 |||||

RESULT 38
 T19214
 UDP-glucose-glycoprotein glucosyltransferase (EC 2.4.1.-) precursor F26H9.8 - Caenorhab
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T19214; T21444
 R:Barlow, K.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19091
 A:Accession: T19214
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1377 <WIL>
 A:Cross-references: UNIPROT:P01854; EMBL:Z81467; PIDN:CAB03874.1; GSPDB:GN000019; CESP:F2
 A:Experimental source: clone C12C8
 R:Baynes, C.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19422
 A:Accession: T21444
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1377 <W12>

A:Cross-references: EMBL:Z81516; PIDN:CAB04207.1; GSPDB:GN000019; CESP:F26H9.8
 A:Experimental source: clone F26H9
 C:Genetics:
 A:Gene: CESP:F26H9.8
 A:Map position: 1
 A:Introns: 40/2; 70/1; 152/2; 318/2; 429/3; 494/2; 538/3; 564/3; 625/3; 654/3; 782/3; 822/3
 C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase

Query Match 2.5%; Score 7; DB 2; Length 1377;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 NLHLRNG 172
 DB 1014 NLHLRNG 1020
 |||||

RESULT 39
 T3236
 hypothetical protein T10H9.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T3236
 R:Greco, T.; Bradshaw, H.; O'Brien, D.
 submitted to the EMBL Data Library, May 1998
 A:Description: The sequence of C. elegans cosmid T10H9.
 A:Reference number: Z21306
 A:Accession: T3236
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1414 <GRE>
 A:Cross-references: UNIPROT:O76411; EMBL:AF067949; PIDN:AAC19236.1; GSPDB:GN000023; CESP:J
 A:Experimental source: strain Bristol N2; clone T10H9
 C:Genetics:
 A:Gene: CESP:T10H9.2
 A:Map position: 5
 A:Introns: 56/3; 76/1; 101/1; 161/1; 196/1; 226/3; 269/2; 318/1; 364/1; 475/3; 520/2; 561/2

Query Match 2.5%; Score 7; DB 2; Length 1414;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 RGPQVRA 123
 DB 1110 RGPQVRA 1116
 |||||

RESULT 40
 E64477
 replication factor C homolog - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: E64477
 R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.; Reisch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: E64477
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1847 <BUL>
 A:Cross-references: UNIPROT:Q58817; GB:U67583; GB:L77117; NID:92826409; PIDN:AAB99433.1;
 C:Genetics:
 A:Map position: REV1393176-1387633
 A:Start codon: TTG

Query Match 2.5%; Score 7; DB 2; Length 1847;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 IPFELKEN 253

Db 877 IPFELKEN 883

RESULT 41

T43262

calcium channel alpha-1 chain, L-type - Stylophora pistillata

C:Species: Stylophora pistillata

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T43262

R:Zoccola, D.; Tambutte, E.; Senegas-Balazs, F.; Michiels, J.F.; Failla, J.P.; Jaubert, J.

Gene 227, 157-167, 1999

A:Title: Cloning of a calcium channel alpha1 subunit from the reef-building coral, Stylo

A:Reference number: 222375; MUID:99148007; PMID:10023047

A:Accession: T43262

A:Status: preliminary;

A:Molecule type: mRNA

A:Residues: 1-1891 <ZOC>

A:Cross-references: UNIPROT:O97017; EMBL:U64465; NID:g4204977; PID:g4204978; PIDN:AA114

C:Genetics:

A:Gene: CACHL

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 2.5%; Score 7; DB 2; Length 1891;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 FLKEDDS 63

Db 1621 FLKEDDS 1627

RESULT 42

B81192

hemagglutinin/hemolysin-related protein NMB0497 [imported] - Neisseria meningitidis (str

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: B81192

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: B81192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1975 <TET>

A:Cross-references: UNIPROT:Q9K0S7; GB:AE002406; GB:AE002098; NID:g7225720; PIDN:AAF4092

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0497

Query Match 2.5%; Score 7; DB 2; Length 1975;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129

Db 557 AAHITGT 563

RESULT 43

G81044

hemagglutinin/hemolysin-related protein NMB1779 [imported] - Neisseria meningitidis (str

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: G81044

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: G81044

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1995 <TET>

A:Cross-references: UNIPROT:Q9JY23; GB:AE002527; GB:AE002098; NID:g7227023; PIDN:AAF4211;

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB1779

Query Match 2.5%; Score 7; DB 2; Length 1995;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129

Db 560 AAHITGT 566

RESULT 44

B81989

hypothetical protein NMA0688 [imported] - Neisseria meningitidis (strain Z2491 serogroup

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C:Accession: B81989

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel]

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: B81989

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2015 <PAS>

A:Cross-references: UNIPROT:Q9JRD2; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CA83974

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA0688

Query Match 2.5%; Score 7; DB 2; Length 2015;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129

Db 560 AAHITGT 566

RESULT 45

GNWVW

genome polypeptide - Murray Valley encephalitis virus (strain Australia)

N:Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS1

a; nonstructural protein NS4b; nonstructural protein NS5

C:Species: Murray Valley encephalitis virus

C:Date: 30-Jun-1988 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004

C:Accession: A24635; A60288

R:Dalgarno, L.; Trent, D.W.; Strauss, J.H.; Rice, C.M.

J. Mol. Biol. 187, 309-323, 1986

A:Title: Partial nucleotide sequence of the Murray Valley encephalitis virus genome: com

A:Reference number: A24635; MUID:86200215; PMID:3009829

A:Accession: A24635

A:Molecule type: genomic RNA

A:Residues: 1-1780 <DAL>

A:Cross-references: UNIPROT:P05769; GB:X03467; NID:g59329; PIDN:CAA27184.1; PID:g755731

R:Lee, E.; Fernon, C.; Simpson, R.; Weir, R.C.; Rice, C.M.; Dalgarno, L.

Virus Genes 4, 197-213, 1990

A:Title: Sequence of the 3' half of the Murray Valley encephalitis virus genome and map

A:Reference number: A60288; MUID:91102934; PMID:1702914

A:Accession: A60288

A:Molecule type: genomic RNA

A:Residues: 1504-1778,'V',1780-3434 <LEE>
 C:Superfamily: yellow fever virus genome polyprotein
 C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
 F:1-125/Product: capsid protein #status predicted <CAP>
 F:126-292/Product: membrane protein precursor #status predicted <GLC>
 F:126-217/Domain: terminal signal sequence #status predicted <SIG>
 F:218-292/Product: membrane protein #status predicted <GLM>
 F:278-292/Domain: transmembrane #status predicted <TN1>
 F:293-793/Product: envelope protein #status predicted <ENV>
 F:773-791/Domain: transmembrane #status predicted <TN2>
 F:794-1205/Product: nonstructural protein NS1 #status predicted <NS1>
 F:1206-1372/Product: nonstructural protein NS2a #status predicted <NS2a>
 F:1373-1503/Product: nonstructural protein NS2b #status predicted <NS2b>
 F:1504-2122/Product: nonstructural protein NS3 #status predicted <NS3>
 F:1697-1704/Region: nucleotide-binding motif A (P-loop)
 F:1784-1789/Region: nucleotide-binding motif B
 F:1788-1791/Region: DEAH motif
 F:2123-2414/Product: nonstructural protein NS4a #status predicted <NS4a>
 F:2415-2529/Product: nonstructural protein NS4b #status predicted <NS4b>
 F:2530-3434/Product: nonstructural protein NS5 #status predicted <NS5>
 F:73,140,446/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.5%; Score 7; DB 1; Length 3434;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 VIFTVLL 26
 |||||
 DB 278 VIFTVLL 284

RESULT 46
 T04365
 ethylene responsive element binding protein - rice
 C:Species: Oryza sativa (rice)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T04365
 R:Kim, C.Y.; Jeong, S.Y.; Choe, M.S.; Cheong, Y.H.; Han, C.D.; Cho, M.J.
 submitted to the EMBL Data Library, March 1997
 A:Description: Isolation and characterization of early inducible rice genes by a fungal
 A:Reference number: Z15314
 A:Accession: T04365
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-47 <KIM>
 A:Cross-references: UNIPROT:O24522; EMBL:U95216; NID:g2443456; PIDN:RAB71382.1; PID:g244

C:Genetics: EREBP1
 A:Gene: EREBP1

Query Match 2.1%; Score 6; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 VLLQSL 29
 |||||
 DB 2 VLLQSL 7

RESULT 47
 S78202
 H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - fission yeast (Schizosacchar

C:Species: mitochondrion Schizosaccharomyces pombe
 C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 03-Jun-2002
 C:Accession: S78202
 R:Lang, B.F.

submitted to the EMBL Data Library, August 1990
 A:Description: The mitochondrial genome of the fission yeast Schizosaccharomyces pombe:
 chizosaccharomyces pombe and Aspergillus nidulans.
 A:Reference number: S78195
 A:Accession: S78202
 A:Molecule type: DNA
 A:Residues: 1-48 <LAN>
 A:Cross-references: EMBL:X54421; NID:g13639; PID:g1334456

A:Experimental source: strain ad7-50h

C:Genetics:
 A:Gene: atp8
 A:Genome: mitochondrion
 A:Genetic code: SGC2
 C:Superfamily: yeast H+-transporting ATP synthase protein 8
 C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxid

Query Match 2.1%; Score 6; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 IFTVLL 26
 |||||
 DB 19 IFTVLL 24

RESULT 48
 AF2105
 hypothetical protein asl2397 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AF2105
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AF2105
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-55 <KUR>
 A:Cross-references: UNIPROT:O8YUF3; GB:BA000019; PIDN:BA074096.1; PID:g17131489; GSPDB:G

A:Experimental source: strain PCC 7120

C:Genetics:
 A:Gene: asl2397

Query Match 2.1%; Score 6; DB 2; Length 55;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 FLSNLH 168
 |||||
 DB 35 FLSNLH 40

RESULT 49
 C60157
 hypothetical protein 2 (prtM 5' region) - Lactococcus lactis subsp. cremoris plasmid pMW
 C:Species: Lactococcus lactis subsp. cremoris
 C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
 C:Accession: C60157
 R:Haandrikman, A.J.; van Leeuwen, C.; Kok, J.; Vos, P.; de Vos, W.M.; Venema, G.
 Appl. Environ. Microbiol. 56, 1890-1896, 1990
 A:Title: Insertion elements on lactococcal proteinase plasmids.
 A:Reference number: A60157; MUID:90343335; PMID:2166472
 A:Accession: C60157
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-56 <HAA>
 A:Cross-references: UNIPROT:Q48684; GB:M37396; NID:g149472; PIDN:AAA25212.1; PID:g149474

Query Match 2.1%; Score 6; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 VLLQSL 29
 |||||
 DB 39 VLLQSL 44

RESULT 50
C97621
hypothetical protein AGR_C_3957 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: C97621
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: C97621
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-62 <KUR>
A/Cross-references: UNIPROT:Q8U558; GB:AB007869; PIDN:AAK87924.1; PID:gl5157324; GSPDB:G
C/Genetics:
A/Gene: AGR_C_3957
A/Map position: circular chromosome

Query Match 2.1%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 118 GQORVA 123
Db 7 GQORVA 12

RESULT 51
AG0025
probable bacterioferritin-associated ferredoxin bfd [imported] - Yersinia pestis (strain
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AG0025
R/Parthill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AG0025
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-64 <KUR>
A/Cross-references: UNIPROT:Q8ZJB1; GB:AL590842; PIDN:CAC89066.1; PID:gl5978306; GSPDB:G
C/Genetics:
A/Gene: bfd
C/Superfamily: yheA protein

Query Match 2.1%; Score 6; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 QLRQLV 88
Db 28 QLRQLV 33

RESULT 52
AC0774
hypothetical protein STY2363 [imported] - Salmonella enterica subsp. enterica serovar Ty
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AC0774
R/Farkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AC0774
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-65 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD02513.1; PID:gl6503375; GSPDB:GN00176
C/Genetics:
A/Gene: STY2363

Query Match 2.1%; Score 6; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 196 IKENTK 201
Db 46 IKENTK 51

RESULT 53
C91249
hypothetical protein ECe4963 [imported] - Escherichia coli (strain O157:H7, substrain RI
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: C91249
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
Gawawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: C91249
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-85 <HAY>
A/Cross-references: UNIPROT:Q8X322; GB:BA000007; PIDN:BA838386.1; PID:gl13364439; GSPDB:G
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: ECe4963

Query Match 2.1%; Score 6; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 105 EKOONI 110
Db 31 EKOONI 36

RESULT 54
S78744
protein YDR363w-a - yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 09-Jul-2004
C/Accession: S78744
R/Du, Z.
Submitted to the EMBL Data Library, June 1995
A/Description: The sequence of S. cerevisiae cosmid 9476.
A/Reference number: S61148
A/Accession: S78744
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-89 <DUZ>
A/Cross-references: UNIPROT:O94742; EMBL:U28372; MIPS:YDR363w-a
C/Genetics:
A/Gene: SGD:HOD1
A/Cross-references: SGD:S0007235
A/Map position: 4R

Query Match 2.1%; Score 6; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 FTNELK 43

Db 73 FTNELK 78

RESULT 55

B82311 conserved hypothetical protein VC0527 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1) [text_change 09-Jul-2004]

C:Species: *Vibrio cholerae*

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: B82311

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, J.L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035; PMID:20406833; PMID:10952301

A:Accession: B82311

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-96 <HEI>

A:Cross-references: UNIPROT:Q9KJ3; GB:AE004139; GB:AE003852; NID:g9654953; PIDN:AAF9369

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0527

A:Map position: 1

C:Superfamily: hypothetical protein HI0673

Query Match 2.1%; Score 6; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 NLHRLN 171

|||||

Db 47 NLHRLN 52

RESULT 56

AE3205 transposase tnp [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont) plasmid AT

C:Species: *Agrobacterium tumefaciens*

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: AE3205

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wooley, G.; Gillet, W.; Grant, C.; Guenther, T.; Kutayavin, T.; Levy, R.; Li, M.; McClelland, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Title: The genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A:Reference number: AE3257; PMID:21608550; PMID:11743193

A:Accession: AE3205

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-96 <KUR>

A:Cross-references: UNIPROT:Q8UUV4; GB:AE008687; PIDN:AAU46059.1; PID:g17743819; GSPDB:G

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: tnp

A:Genome: plasmid

Query Match 2.1%; Score 6; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 LVRERG 118

|||||

Db 17 LVRERG 22

RESULT 57

G91248 hypothetical protein ECs4959 [imported] - *Escherichia coli* (strain O157:H7, substrain R1)

C:Species: *Escherichia coli*

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: G91248

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic comparisons with other *Escherichia coli* serotypes

A:Reference number: A99629; PMID:21156231; PMID:11258796

A:Accession: G91248

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <HAY>

A:Cross-references: UNIPROT:Q8X328; GB:BA000007; PIDN:BAE38382.1; PID:g13364435; GSPDB:G

A:Experimental source: strain O157:H7, substrain R1MD 0509952

C:Genetics:

A:Gene: ECs4959

Query Match 2.1%; Score 6; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 SFFGAF 278

|||||

Db 15 SFFGAF 20

RESULT 58

C95337 probable cytochrome C fragment [imported] - *Sinorhizobium meliloti* (strain 1021) magapla

C:Species: *Sinorhizobium meliloti*

C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: C95337

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowsa, K.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti* genome

A:Reference number: A95262; PMID:21396509; PMID:11481432

A:Accession: C95337

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-102 <KUR>

A:Cross-references: UNIPROT:Q92Z89; GB:AE006469; PIDN:AAK65261.1; PID:g14523712; GSPDB:G

A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hymen, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, H.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.

A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A:Reference number: A96039; PMID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: SWall13

A:Genome: plasmid

Query Match 2.1%; Score 6; DB 2; Length 102;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 VAAHIT 127

|||||

Db 96 VAAHIT 101

RESULT 59

E69832 conserved hypothetical protein yhgB - *Bacillus subtilis*

N:Alternate names: hypothetical protein Y (pbpf 5' region)

C:Species: *Bacillus subtilis*

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: E69832; C40614

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Eppington, J.; Fabret, J.; Ferrari, E.

Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen-
iech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E59832
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-104 <KUN>
A;Cross-references: UNIPROT:P38048; GB:Z99109; GB:AL009136; NID:g2633260; PIDN:CAB12849.
A;Experimental source: strain 168
R;Popham, D.L.; Setlow, P.
J. Bacteriol. 175, 4870-4876, 1993
A;Title: Cloning, nucleotide sequence, and regulation of the *Bacillus subtilis* pbpF gene
A;Reference number: A40614; MUID:93328693; PMID:8335642
A;Accession: C40614
A;Molecule type: DNA
A;Residues: 1-67 <POP>
A;Cross-references: GB:LI0630
A;Genetics:
A;Gene: yhgB

Query Match 2.1%; Score 6; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 222 LMKSR 227
Db 25 LMKSR 30
|||||

RESULT 60
B86818
hypothetical protein ypiJ [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
C;Species: *Lactococcus lactis* subsp. *lactis*
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86818
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s
A;Reference number: A86825; MUID:21235186; PMID:11337471
A;Accession: B86818
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <STO>
A;Cross-references: UNIPROT:Q9CFD5; GB:AE005176; PID:g12724547; PIDN:AAK05644.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ypiJ

Query Match 2.1%; Score 6; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 137 SSPNSK 142
Db 42 SSPNSK 47
|||||

RESULT 61
S09964
IG kappa chain V-J region (105-2H) - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: S09964

R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
A;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09964
A;Molecule type: mRNA
A;Residues: 1-107 <REI>
A;Cross-references: EMBL:X51852; NID:g55393; PIDN:CAA36145.1; PID:g930229
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMW>

Query Match 2.1%; Score 6; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 99 TISTVQ 104
Db 74 TISTVQ 79
|||||

RESULT 62
A44887
glucose transporter isoform 1, GLUT 1 - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 24-Sep-1999
C;Accession: A44887
R;Hogan, A.; Heyner, S.; Charron, M.J.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; The
Development 113, 363-372, 1991
A;Title: Glucose transporter gene expression in early mouse embryos.
A;Reference number: A44887; MUID:92111400; PMID:1765007
A;Accession: A44887
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <HOG>
A;Cross-references: GB:S77924; NID:g242127; PIDN:AAB20846.1; PID:g242128
A;Experimental source: embryo
A;Note: this sequence is inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:77924, NCBI:P:77925)
C;Superfamily: glucose transport protein

Query Match 2.1%; Score 6; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 IFTVLL 26
Db 80 IFTVLL 85
|||||

RESULT 63
F84012
hypothetical protein BH2902 [imported] - *Bacillus halodurans* (strain C-125)
C;Species: *Bacillus halodurans*
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F84012
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84012
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <STO>
A;Cross-references: UNIPROT:Q9K8V0; GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA0667
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2902

Query Match 2.1%; Score 6; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 99 TISTVQ 104
Db 74 TISTVQ 79
|||||

QY 170 RINGELV 175
 Db 38 RINGELV 43
 RESULT 64
 AC2887
 conserved hypothetical protein Atu2536 [imported] - Agrobacterium tumefaciens (strain C58)
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AC2887
 C:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AC2887
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-112 <KUR>
 A:Cross-references: UNIPROT:Q8UCG1; GB:AE008689; PIDN:AAAL43513.1; PID:gl17741022; GSPDB:G
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu2526
 A:Map position: circular chromosome
 Query Match 2.1%; Score 6; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 168 HLRNGE 173
 Db 35 HLRNGE 40
 RESULT 65
 H97662
 hypothetical protein AGR_C_4590 [imported] - Agrobacterium tumefaciens (strain C58, Cere
 C:Species: Agrobacterium tumefaciens
 C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: H97662
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: H97662
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-112 <KUR>
 A:Cross-references: UNIPROT:Q8UCG1; GB:AE007869; PIDN:AAK8257.1; PID:gl15157717; GSPDB:G
 C:Genetics:
 A:Gene: AGR_C_4590
 A:Map position: circular chromosome
 Query Match 2.1%; Score 6; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 168 HLRNGE 173
 Db 35 HLRNGE 40
 RESULT 66
 B25924
 Ig kappa chain precursor V region (Ser-b) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
 C:Accession: B25924

R:Boyd, R.T.; Goldrick, M.M.; Gottlieb, P.D.
 Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138, 1986
 A:Title: Structural differences in a single gene encoding the V-kappa-Ser group of light
 A:Reference number: A94141; MUID:87067464; PMID:3097643
 A:Accession: B25924
 A:Molecule type: DNA
 A:Residues: 1-115 <BOY>
 A:Cross-references: GB:M14360; NID:gl197464; PIDN:AAA39034.1; PID:gl197465
 A:Experimental source: strain BALB/C
 C:Genetics:
 A:introns: 17/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-115/Product: Ig kappa chain V region Ser-b #status predicted <MAT>
 F:36-110/Domain: immunoglobulin homology <IMM>
 Query Match 2.1%; Score 6; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 99 TISTVQ 104
 Db 94 TISTVQ 99
 RESULT 67
 C83166
 probable chaperone PA3842 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: C83166
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
 A:Reference number: AB2950; MUID:20437337; PMID:10984043
 A:Accession: C83166
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-116 <STO>
 A:Cross-references: UNIPROT:Q51450; GB:AE004801; GB:AE004091; NID:g9950011; PIDN:AG0722;
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA3842
 C:Superfamily: Yersinia pestis plasmid pCD1 hypothetical protein syce
 Query Match 2.1%; Score 6; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 67 PNDEES 72
 Db 21 PNDEES 26
 RESULT 68
 F97174
 hypothetical protein CAC2228 [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C:Accession: F97174
 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: F97174
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-117 <KUR>
 A:Cross-references: UNIPROT:Q97GY7; GB:AE001437; PIDN:AAK80185.1; PID:gl15025227; GSPDB:G

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC2228

Query Match 2.1%; Score 6; DB 2; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 NGELVI 176

Db 91 NGELVI 96

RESULT 69

QJQ2032

lambda 208 protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus

C;Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OPMNPV

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C;Accession: JQ2032

R;Russell, R.L.Q.; Rohrmann, G.F.

J. Gen. Virol. 74, 1191-1195, 1993

A;Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsugata

A;Reference number: PQ0633; MUID:93286576; PMID:8389803

A;Accession: JQ2032

A;Molecule type: DNA

A;Residues: 1-119 <RUS>

A;Cross-references: UNIPROT:Q05122; DDBJ:D13375; NID:G222217; PIDN:BA02641.1; PID:G222217

C;Superfamily: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus lambda 208 protein

Query Match 2.1%; Score 6; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QLRQLV 88

Db 90 QLRQLV 95

RESULT 70

D89803

conserved hypothetical protein SA0358 [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: D89803

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: D89803

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-122 <KUR>

A;Cross-references: UNIPROT:Q99WK6; GB:BA000018; PID:gl3700285; PIDN:BA041583.1; GSPDB:G

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA0358

Query Match 2.1%; Score 6; DB 2; Length 122;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KEDDSY 64

Db 42 KEDDSY 47

RESULT 71

AH0043

probable lipoprotein YPO0352 [imported] - Yersinia pestitis (strain CO92)

C;Species: Yersinia pestitis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AH0043

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E

Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestitis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AH0043

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-128 <KUR>

A;Cross-references: UNIPROT:Q8ZIV2; GB:AL590842; PIDN:CAC89211.1; PID:gl5978450; GSPDB:GN

C;Genetics:

A;Gene: YPO0352

C;Superfamily: Escherichia coli hypothetical protein o128

Query Match 2.1%; Score 6; DB 2; Length 128;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSS 138

Db 35 SNTLSS 40

RESULT 72

D64559

hypothetical protein HP0316 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C;Accession: D64559

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N

A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: D64559

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-130 <TOM>

A;Cross-references: UNIPROT:Q25085; GB:AE000549; GB:AE000511; NID:g2313403; PIDN:AA00738;

Query Match 2.1%; Score 6; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 FTNELK 43

Db 111 FTNELK 116

RESULT 73

F86829

ribose ABC transporter permease protein rbad [imported] - Lactococcus lactis subsp. lactis

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C;Accession: F86829

R;Solotkin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp.

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: F86829

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-132 <STO>

A;Cross-references: UNIPROT:Q9CF43; GB:AE005176; PID:gl2724648; PIDN:AAK05736.1; GSPDB:GN

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: rbad

C;Superfamily: fucose operon U protein

Job time : 46 secs

Query Match 2.1%; Score 6; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 EBIKEN 199
Db 71 EBIKEN 76

RESULT 74

F70650
hypothetical protein RV3069 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: F70650
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A: Authors: Scares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A: Reference number: A70500; MUID:98295987; PMID:9634230
A: Accession: F70650
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-132 <COL>
A: Cross-references: UNIPROT:P95089; GB:283866; GB:AL123456; NID:g3261691; PIDN:CAB06254.
A: Experimental source: strain H37RV
C: Genetics:
A: Gene: RV3069
C: Superfamily: hypothetical protein MJ1523

Query Match 2.1%; Score 6; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 GAFLVG 281
Db 48 GAFLVG 53

RESULT 75

AC0855
probable regulatory protein STY3045 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A: Note: this species has also been called Salmonella typhi
C: Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C: Accession: AC0855
R: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, M.; Connor, R.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A: Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A: Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Paratyphi C
A: Reference number: AB0502; MUID:21534947; PMID:11677608
A: Accession: AC0855
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-134 <PAR>
A: Cross-references: GB:AL513382; PIDN:CAD06026.1; PID:gl6503993; GSPDB:GN00176
C: Genetics:
A: Gene: STY3045

Query Match 2.1%; Score 6; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 QLVRKM 91
Db 127 QLVRKM 132

Search completed: June 22, 2005, 06:52:39

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2005, 06:07:26 ; Search time 175 Seconds
(without alignments)
822.253 Million cell updates/sec

Title: US-10-662-429-2
Perfect score: 281
Sequence: 1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFIVG 281

Scoring table:
OLIGO
Gapop-60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	281	100.0	281	1 TN10 HUMAN
2	52	18.5	63	2 Q6JSD9
3	29	10.3	287	2 Q8K3G0
4	14	5.0	291	1 TN10 MOUSE
5	13	4.6	304	2 Q7TIF2
6	10	3.6	299	2 Q6DHG9
7	8	2.8	155	2 Q64UG5
8	8	2.8	465	2 Q9HKC2
9	8	2.8	473	2 Q8FUC2
10	8	2.8	474	2 Q6LQD8
11	8	2.8	475	2 Q8S6N3
12	8	2.8	643	2 Q9R293
13	8	2.8	939	2 Q9NG57
14	8	2.8	950	2 Q15788
15	8	2.8	1248	2 Q8IBZ8
16	7	2.5	39	2 Q95NV2
17	7	2.5	51	1 INS ORNAN
18	7	2.5	73	2 Q7URQ9
19	7	2.5	88	2 Q8KH11
20	7	2.5	92	2 Q87OH0
21	7	2.5	93	2 Q9HSN3
22	7	2.5	94	2 Q8PMD7
23	7	2.5	96	1 AH4 TOXGO
24	7	2.5	106	2 Q9LJ97
25	7	2.5	107	2 Q9Y777
26	7	2.5	112	2 Q932M3
27	7	2.5	121	2 Q7U9A5
28	7	2.5	123	2 Q6V7H3
29	7	2.5	125	2 P72087
30	7	2.5	134	2 Q8MM82
31	7	2.5	155	2 Q9YBC2
				P50591 homo sapien
				Q6JSD9 homo sapien
				Q8K3G0 rattus norv
				P50592 mus musculus
				Q7TIF2 gallus gall
				Q6DHG9 brachydanio
				Q64UG5 bacteroides
				Q9HKC2 thermoplasma
				Q8FUC2 corynebacte
				Q6LQD8 photobacter
				Q8S6N3 oryza sativ
				Q9R293 deinococcus
				Q9NG57 plasmodium
				Q15788 plasmodium
				Q8IBZ8 plasmodium
				Q95NV2 drosophila
				Q9TG7 ornithorhyn
				Q7URQ9 rhodopirell
				Q8KH11 bacillus th
				Q87OH0 saccharomyc
				Q9HSN3 halobacteri
				Q8PMD7 xanthomonas
				Q27001 toxoplasma
				Q9LV97 arabidopsis
				Q9Y777 sulfolobus
				Q932M3 staphylococ
				Q7U9A5 synchococc
				Q6V7H3 equus cabal
				P72087 neisseria m
				Q8MM82 caenorhabdi
				Q9YBC2 aeropyrum p

ALIGNMENTS

Q83TUL staphylococ
Q6GBC3 staphylococ
Q6GBC3 staphylococ
Q9N8D4 trypanosoma
Q7R3Y3 giardia lam
Q8P7K6 xanthomonas
Q8P1X9 xanthomonas
Q82UJ6 nitrosomona
Q75496 homo sapien
Q91TD0 arabidopsis
Q6S8A0 acidovorax
Q6S8A0 acidovorax
Q7MMP6 vibrio vuln
Q8DFN8 bacillus ce
Q72XY8
P90611 toxoplasma
Q7PV53 anopheles g
Q99R85 staphylococ
Q7A004 staphylococ
Q6G6H6 staphylococ
Q94262 schizosacch
Q98D64 rhizobium l
Q636T1 bacillus ce
Q81WU0 bacillus an
Q6HF64 bacillus th
Q8R0L0 mus musculu
Q82J67 chlamydophi
Q8DXW4 streptococc
Q8E3I3 streptococc
Q6KZP1 picophilus
Q6Z6A7 oryza sativ
Q96QL7 homo sapien
Q9VJ33 drosophila
Q9PEN6 xylella fas
Q9ZKY9 helicobacte
Q7VJZ3 helicobacte
Q84846 chlamydia t
Q9P180 chlamydia m
Q9AVE6 oryza sativ
Q98AU0 xenopus lae
P90756 caenorhabdi
Q8WJ2 mytilus edu
Q6G1F3 xenopus tro
Q6C774 kluyveromyc
Q7U3W6 synchococc
Q8TWS8 methanopyru
Q915E1 salmonella
Q6F9A2 acinetobact
Q89W4 bradyrhizob
Q7N5Q0 photorhabdu
Q91TH1 arabidopsis
Q68SS3 pleurotus d
Q68SS2 pleurotus d
Q87CC1 xylella fas
Q9PCZ3 xylella fas
Q9H766 homo sapien
Q9UX27 sulfolobus
Q6GPT4 xenopus lae
Q8NZ26 streptococc
Q99XN8 streptococc
Q8K5J7 streptococc
Q8S179 oryza sativ
Q8K1R0 pseudomonas
Q8KIU0 pseudomonas

157 2 Q83TUL
157 2 Q6GBC3
157 2 Q6GBC3
172 2 Q9N8D4
191 2 Q7R3Y3
193 1 Y005_XANCP
193 1 YR66_XANAC
204 1 LIPB_NITEU
209 1 GEMI_HUMAN
217 2 Q91TD0
220 2 Q6S8A0
220 2 Q6S8A0
222 2 Q7MMP6
222 2 Q8DFN8
230 2 Q72XY8
231 2 P90611
232 2 Q7PV53
232 2 Q6S8B3
240 1 CD7_HUMAN
240 2 Q64MD3
247 2 Q9EZK4
247 2 Q99RD5
247 2 Q7A004
247 2 Q7A3K0
247 2 Q6G6H6
251 2 Q94262
253 2 Q98D64
271 2 Q636T1
271 2 Q81WU0
271 2 Q6HF64
293 2 Q8R0L0
296 1 LGT_CHLCV
298 2 Q8DXW4
298 2 Q8E3I3
305 2 Q6KZP1
314 2 Q6Z6A7
318 2 Q96QL7
322 2 Q9VJ33
327 2 Q9PEN6
329 2 Q9ZKY9
343 2 Q7VJZ3
354 2 Q84846
354 2 Q9P180
359 2 Q9AVE6
361 2 Q98SU0
362 1 YE1J_CAEEL
367 1 MANA_MYTED
367 2 Q6GLF3
374 2 Q6C774
374 2 Q7U3W6
375 2 Q8TWS8
375 2 Q915E1
376 2 Q6F9A2
376 2 Q89SW4
379 2 Q7N5Q0
383 2 Q91TH1
389 2 Q68SS3
395 2 Q68SS2
396 2 Q87CC1
401 2 Q9PCZ3
402 2 Q9H766
404 2 Q9UX27
405 2 Q6GPT4
406 2 Q8NZ26
406 2 Q99XN8
406 2 Q8K5J7
414 2 Q8S179
417 2 Q8K1R0
417 2 Q8KIU0

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RESULT 1

NT10 HUMAN

ID TN10 HUMAN STANDARD; PRT; 281 AA.

AC P50591;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 10 (TNF-related

DE apoptosis-inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).

GN Name=TNFSF10; Synonyms=APO2L, TRAIL;

OS Homo sapiens (Human).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

SEQUENCE FROM N.A.

RP MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;

RX Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,

RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,

RA Goodwin R.G.;

RT "Identification and characterization of a new member of the TNF family

RT that induces apoptosis.";

RL Immunity 3:673-682(1995).

RN [2]

SEQUENCE FROM N.A.

RP TISSUE=Placenta;

RX MEDLINE=96278649; PubMed=86631110; DOI=10.1074/jbc.271.22.12687;

RA Pitti R.W., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,

RA Ashkenazi A.;

RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor

RT necrosis factor cytokine family.";

RL J. Biol. Chem. 271:12687-12690(1996).

RN [3]

SEQUENCE FROM N.A.

RP TISSUE=Lymph;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [4]

X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.

RX PubMed=10542098; DOI=10.1038/14935;

RA Mongkolkeapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,

RA Jones E.Y., Screaton G.R.;

RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring

RT specificity in apoptotic initiation.";

RL Nat. Struct. Biol. 6:1048-1053(1999).

[6]

RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.

RX MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;

RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,

RA Sung Y.C., Oh B.-H.;

RT "2.8 Å resolution crystal structure of human TRAIL, a cytokine with

RT selective antitumor activity.";

RL Immunity 11:253-261(1999).

CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,

CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and

CC possibly also to TNFRSF10F/OPG. Induces apoptosis. Its activity

CC may be modulated by binding to the decoy receptors

CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF10B/OPG that cannot

CC induce apoptosis.

CC -!- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per

CC trimer.

CC -!- SUBUNIT: Homotrimer.

CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung

CC and prostate.

CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

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CC or send an email to license@isb-sib.ch).

CC

DR EMBL; U37518; AAC50332.1; -

DR EMBL; U57059; AAB01233.1; -

DR EMBL; BC032722; AAH32722.1; -

DR PDB; 1D0G; X-ray; A/B/D-114-281.

DR PDB; 1D2Q; X-ray; A-114-281.

DR PDB; 1D4V; X-ray; B-119-281.

DR PDB; 1D66; X-ray; A-91-281.

DR PDB; 1DU3; X-ray; D/E/F/J/K/L-114-281.

DR Genew; HGNC:11925; TNFSF10.

DR H-InvDB; HIX0003863; -

DR MIM; 603598; -

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0005625; C:soluble fraction; TAS.

DR GO; GO:0005102; F:receptor binding; TAS.

DR GO; GO:0007267; P:cell-cell signaling; TAS.

DR GO; GO:0006917; P:induction of apoptosis; TAS.

DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB; IEP.

DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR006052; TNF family.

DR InterPro; IPR008983; TNF-like.

DR InterPro; IPR003636; TNF_subf.

DR Pfam; PF00229; TNF; 1.

DR ProDom; PD002012; TNF_subf; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF 1; 1.

DR PROSITE; PS00049; TNF 2; 1.

KW 3D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor;

KW Transmembrane; Zinc.

FT DOMAIN 1 17 Cytoplasmic (Potential).

FT TRANSMEM 18 38 Signal-anchor for type II membrane

FT protein (Potential).

FT FT Extracellular (Potential).

FT FT Zinc.

FT DOMAIN 39 281

FT METAL 230 230

FT STRAND 123 127

FT STRAND 149 150

FT STRAND 163 165

FT STRAND 167 170

FT TURN 171 172

FT TURN 173 176

FT STRAND 180 193

FT TURN 198 199

FT STRAND 205 213

FT STRAND 220 228


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FT TURN 233 234
FT STRAND 237 250
FT TURN 252 253
FT STRAND 255 260
FT HELIX 263 265
FT STRAND 266 267
FT TURN 270 272
FT STRAND 274 279
SQ SEQUENCE 281 AA; 32509 MW; DDAAF78DAAB2F6D CRC64;

Query Match 100.0%; Score 281; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-287;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEQGSLSGTCVLIVFTVLLQSLCAVATYVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMVEQGSLSGTCVLIVFTVLLQSLCAVATYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDESNMSPCWQVKWQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDPNDESNMSPCWQVKWQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
DB 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
QY 181 FYIYISQTYPRFOEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSNCSWDAEYGLY 240
DB 181 FYIYISQTYPRFOEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSNCSWDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 2
Q6JSD9 PRELIMINARY; PRT; 63 AA.
AC Q6JSD9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine tumor necrosis factor ligand superfamily member 10
DE (Fragment).
GN Name=TNFSF10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RA Polvi A., Ruosaari S., Vendelin J., West A., Saarikko I.,
RA Reinikainen A., Hollmen J., Laitinen T., Mannila H., Laheemaa R.,
RA Kere J.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY312579; AAR16184.1; -
FT NON TER 1 1
SQ SEQUENCE 63 AA; 7638 MW; 8F0C7936DA5AA6E6 CRC64;

Query Match 18.5%; Score 52; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.7e-46;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESNMSPCWQVKWQLRQLVRK 90
DB 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESNMSPCWQVKWQLRQLVRK 52

RESULT 3
Q8K3G0 PRELIMINARY; PRT; 287 AA.
ID Q8K3G0
AC Q8K3G0;
```

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE TNF-related apoptosis inducing ligand.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA;
RA Mueller A.M., Giegerich G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY115578; AAM49797.1; -
DR HSSP; PS0591; ID2Q.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; UNKNOWN_1.
DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;

Query Match 10.3%; Score 29; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 KQMVQYIYKYTSYPPDPILLMKSNCSWS 232
DB 214 KQMVQYIYKYTSYPPDPILLMKSNCSWS 242

RESULT 4
TN10_MOUSE STANDARD; PRT; 291 AA.
ID TN10_MOUSE
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein).
GN Name=TNFSF10; Synonyms=Trail;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT Identification and characterization of a new member of the TNF family
RT that induces apoptosis."
RL Immunity 3:673-682(1995)
CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC may be modulated by binding to the decoy receptors
CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC induce apoptosis.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Widespread.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----

DR EMBL: U37522; AAC52345.1; -.
DR HSSP: P50591; 1D2Q.
DR MGD: MGI:107414; Tnfef10.
DR InterPro: IPR006052; TNF family.
DR InterPro: IPR008983; TNF-like.
DR InterPro: IPR003636; TNF_subf.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD002012; TNF subf; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF 1; 1.
DR PROSITE: PS50049; TNF 2; 1.
KW Apoptosis; Cytokine; Signal-anchor; Transmembrane.
FT DOMAIN 1 17 Cytoplasmic (Potential).
FT TRANSMEM 18 38 Signal-anchor for type II membrane
FT DOMAIN 39 291 Extracellular (Potential).
FT CARBOHYD 52 52 N-linked (GlcNAc...), (Potential).
SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 5.0%; Score 14; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKTSYDPDI 220
DB 217 VQYIYKTSYDPDI 230
|||||

RESULT 5

Q7TIF2 PRELIMINARY; PRT; 304 AA.
ID Q7TIF2
AC Q7TIF2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor necrosis factor related apoptosis inducing ligand.
GN Names=TRAIL;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;
RA Sayed A., Horiuchi H., Furusawa S., Mateuda H.;
RT "Molecular Cloning and Characterization of Chicken Tumor Necrosis
RT Factor (TNF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis
RT Inducing Ligand (TRAIL).";
RL J. Vet. Med. Sci. 66:643-650 (2004).
DR EMBL: AB114678; BAC79267.1; -.
DR HSSP: P50591; 1D2Q.

DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR006052; TNF family.
DR InterPro: IPR008983; TNF-like.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD002012; TNF_subf; 1.

DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF 1; 1.
DR PROSITE: PS50049; TNF 2; 1.
SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 4.8%; Score 13; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 180 GFYIYSQTYFRF 192
DB 184 GFYIYSQTYFRF 196
|||||

RESULT 6

Q6DHG9 PRELIMINARY; PRT; 299 AA.
ID Q6DHG9
AC Q6DHG9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Zgc:92320.
GN Name=zgc:92320;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Batte F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Whole;
RA Strausberg R.;

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC076005; AAH76005.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR006052; TNF family.
DR InterPro: IPR008983; TNF-like.
DR InterPro: IPR003636; TNF_subf.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD002012; TNF_subf; 1.

DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF 1; 1.
DR PROSITE: PS50049; TNF 2; 1.
SQ SEQUENCE 299 AA; 33526 MW; BA776793D2F11ED5 CRC64;

Query Match 3.6%; Score 10; DB 2; Length 299;

Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0

QY 182 YIYSQTYFR 191
DB 187 YIYSQTYFR 196
|||||

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RESULT 7
Q64UG5
ID Q64UG5 PRELIMINARY; PRT; 155 AA.
AC Q64UG5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE AenC family transcriptional regulator.
GN ORFName=BF2117;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayaishi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0 (2004).
DR EMBL; AF006941; BAD4864.1; -.
KW SEQUENCE 155 AA; 17962 MW; B66A33A8AF0DD863 CRC64;
SQ SEQUENCE 155 AA; 17962 MW; B66A33A8AF0DD863 CRC64;

Query Match 2.8%; Score 8; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 RFQEEIKE 198
DB 84 RFQEEIKE 91
|||||

RESULT 8
Q9HKC2
ID Q9HKC2 PRELIMINARY; PRT; 465 AA.
AC Q9HKC2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical membrane protein.
GN OrderedLocusNames=Ta0679;
OS Thermoplasma acidophilum;
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001; DOI=10.1038/35035069;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513 (2000).
DR EMBL; AL445065; CAC11817.1; -.
DR InterPro; IPR007272; DUF395.
DR Pfam; PF04143; DUF395; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 465 AA; 51450 MW; 7AE47FAFF0C4B5A CRC64;

Query Match 2.8%; Score 8; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 SFFGAFLV 280
DB 402 SFFGAFLV 409
|||||

RESULT 9
Q8FUC2
ID Q8FUC2 PRELIMINARY; PRT; 473 AA.

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AC Q8FUC2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=CE0098;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579 (2003).
DR EMBL; AF052114; BAC16908.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 473 AA; 52745 MW; 9BBF8D8DBAA8E249 CRC64;

Query Match 2.8%; Score 8; DB 2; Length 473;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 LVREGRGP 120
DB 366 LVREGRGP 373
|||||

RESULT 10
Q6LQD8
ID Q6LQD8 PRELIMINARY; PRT; 474 AA.
AC Q6LQD8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative oxidoreductase.
GN Names=ECS3960; OrderedLocusNames=PBPRA2086;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]_
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR378669; CAG20488.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR002114; HPr_SerP_S.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 474 AA; 51903 MW; FA1D1AE8EBPFC95 CRC64;

Query Match 2.8%; Score 8; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLIVITTV 24

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Db      412 VLVIVFTV 419
|||||
RESULT 11
Q8S6N3 PRELIMINARY; PRT; 475 AA.
ID Q8S6N3
AC Q8S6N3
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative kelch-containing protein.
GN ORFNames=OSUNBao0073L01.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feldlyum T.V., Yang Q.Q., Haas B.B., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569(2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092548; AM18732.1; -.
DR EMBL; AB017083; AAP53323.1; -.
DR Gramene; Q8S6N3; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR011043; Gal oxid central.
DR Pfam; PF00646; F-box_1; 2.
DR Pfam; PF01344; Kelch_1; 2.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00612; Kelch; 2.
DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 475 AA; 51606 MW; 84258271A075D2EE CRC64;

Query Match 2.8%; Score 8; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 LSSPNSKN 143
|||||
DB 5 LSSPNSKN 12

RESULT 12
Q9R293 PRELIMINARY; PRT; 643 AA.
ID Q9R293
AC Q9R293
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Drug transport protein, putative.
GN OrderedLocusNames=DRA0061;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;

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OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; Pubmed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001862; AAF12254.1; -.
DR FIR; G75599; G75599.
DR TIGR; DRA0061; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0015520; F: tetracycline:hydrogen antiporter activity; IEA.
DR GO; GO:0005215; F: transporter activity; IEA.
DR GO; GO:0015904; P: tetracycline transport; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR004638; Efflux_EmrB.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR001958; TCR TetA.
DR InterPro; IPR001411; TCR TetB.
DR PRINTS; PR01035; TCRTEA.
DR PRINTS; PR01036; TCRTEB.
DR TIGRFAMs; TIGR00711; efflux_EmrB; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome.
SQ SEQUENCE 643 AA; 67778 MW; 4168A0998E467A63 CRC64;

Query Match 2.8%; Score 8; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLVIVFTV 24
|||||
DB 231 VLVIVFTV 238

RESULT 13
Q9NG57 PRELIMINARY; PRT; 939 AA.
ID Q9NG57
AC Q9NG57
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG1 protein.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Ma C.L., Yu X.B., Shan Z.X., Li X.R.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260819; AAF69519.1; -.
DR InterPro; IPR009011; Manaphp_recept.
SQ SEQUENCE 939 AA; 109367 MW; E896972DC096412D CRC64;

Query Match 2.8%; Score 8; DB 2; Length 939;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140
|||||
DB 373 SNTLSSPN 380

RESULT 14

```

015788 ID Q15788 PRELIMINARY; PRT; 950 AA.

AC Q15788; 950 AA.

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE CG1.

GN Name=cgl;

OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=5833;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HB3;

RX MEDLINE=98054002; PubMed=9393853; DOI=10.1016/S0092-8674(00)80447-X;

RA Su X., Kirkman L.A., Fujitaka H., Wellem T.E.;

RT "Complex polymorphisms in an approximately 330 kDa protein are linked

RT to chloroquine-resistant P. falciparum in Southeast Asia and Africa.";

RL Cell 91:593-603(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=HB3;

RA Su X.-Z., Kirkman L.A., Wellem T.E.;

RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF030690; AAC47851.1; -

DR F01; T09076; T09076.

DR InterPro; IPR009011; Man6php_recept.

SQ SEQUENCE 950 AA; 110601 MW; ED19FEA3B517A378 CRC64;

Query Match 2.8%; Score 8; DB 2; Length 950;

Best Local Similarity 100.0%; Pred. No. 56;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140

DB 361 SNTLSSPN 368

RESULT 15

ID Q8IBZ8 PRELIMINARY; PRT; 1248 AA.

AC Q8IBZ8;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cg1 protein.

GN Name=PF07_0035;

OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=36329;

RN [1]

RP SEQUENCE FROM N.A.

RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,

RA Quail M., Barrall B.;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL844506; CAD50843.1; -

DR InterPro; IPR009011; Man6php_recept.

SQ SEQUENCE 1248 AA; 146629 MW; FDBE0EBF1DF769C2 CRC64;

Query Match 2.8%; Score 8; DB 2; Length 1248;

Best Local Similarity 100.0%; Pred. No. 72;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140

DB 670 SNTLSSPN 677

RESULT 16

Q95NV2 ID Q95NV2 PRELIMINARY; PRT; 39 AA.

AC Q95NV2; 39 AA.

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE GM03003p (GM01206p).

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Friese B., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nuoo J., Facleb J., Paragas V., Park S., Phouanavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY060851; AAL28399.1; -

DR EMBL; AY060825; AAL28373.1; -

DR FlyBase; FBgn0047295; BcDNA:GM01206.

SQ SEQUENCE 39 AA; 4446 MW; 432F8F340E895DC6 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TVVLQSL 29

DB 25 TVVLQSL 31

RESULT 17

INS ORNAN

ID INS ORNAN STANDARD; PRT; 51 AA.

AC Q9TQY7; Q9TQY8;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Insulin.

GN Name=INS;

OS Ornithorhynchus anatinus (Duckbill platypus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.

OX NCBI_TaxID=9258;

RN [1]

RP SEQUENCE.

RC TISSUE=Pancreas;

RX MEDLINE=97021710; PubMed=8868070;

RA Nourae A., Treacy G.B., Shaw D.C., Jeffrey P.D.;

RT "Platyphus insulin: indications from the amino acid sequence of

RT significant differences in structure from porcine insulin.";

RL Biol. Chem. Hoppe-Seyler 377:147-153(1996).

CC -!- FUNCTION: Insulin decreases blood glucose concentration. It

CC increases cell permeability to monosaccharides, amino acids and

CC fatty acids. It accelerates glycolysis, the pentose phosphate

CC cycle, and glycogen synthesis in liver.

CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two

CC disulfide bonds.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the insulin family.

DR PIR; S63591; S63590.

DR HSSP; P01308; 1MHJ.

DR InterPro; IPR004825; Ins/IGF/relax.

DR PRINTS; PR00277; INSULINB.

DR SMART; SM00078; ILGF; 1.

DR PROSITE; PS00262; INSULIN; 1.

KW Direct protein sequencing; Glucose metabolism; Hormone;

KW Insulin family.

KW CHAIN 1 30 Insulin B chain.

FT NON CONS 30 31

FT CHAIN 31 51 Insulin A chain.

FT DISULFID 7 37 Interchain.

FT DISULFID 19 50 Interchain.

FT DISULFID 36 41

```

SQ  SEQUENCE      51 AA;  5854 MW;  0E4D30265D77EAA3 CRC64;

Query Match      2.5%;  Score 7;  DB 1;  Length 51;
Best Local Similarity 100.0%;  Pred.No. 45;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      178  EKGFPYYI 184
          |||||
Db      21  EKGFPYYI 27

RESULT 18
Q7URQ9
ID  Q7URQ9      PRELIMINARY;      PRT;      73 AA.
AC  Q7URQ9;
DT  01-OCT-2003 (TrEMBLrel. 25, Created)
DT  01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  Hypothetical protein.
GN  OrderedLocusNames=RB5505;
OS  Rhodopirellula baltica.
OC  Bacteria; Planctomycetacia; Planctomycetales;
OC  Planctomycetaceae; Firellula.
OX  NCBI_TaxID=117;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1.
RX  MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA  Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA  Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA  Schlesner H., Amann R., Reinhardt R.;
RT  "Complete genome sequence of the marine planctomycete Firellula sp.
RT  strain 1";
RL  Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR  EMBL; BX294142; CAD74279.1; -.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE      73 AA;  8265 MW;  EF2C586B58E7443F CRC64;

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Query Match          2.5%; Score 7; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      223 MKSARNS 229
      |||||
      |||||
DB       1 MKSARNS 7

RESULT 19
Q8KH11
ID Q8KH11 PRELIMINARY; PRT; 88 AA.
DT DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DE Conserved hypothetical membrane protein.
GN GN Name=pBt095;
OS OS Bacillus thuringiensis (subsp. israelensis) .
OC OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX OX NCBI_TaxID=1430;
RN RN [1]
RP RP SEQUENCE FROM N.A.
RX RX MEDLINE=42235415; PubMed=12324359;
RX RX DOI=10.1128/AEM.68.10.5082-5095.2002;
RA RA Berry C., O'Neil S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A.,
RA Harris D., Zaritsky A., Parkhill J.;
RT RT "Complete sequence and organisation of pBtoxis, the toxin-coding
RT plasmid of Bacillus thuringiensis subsp. israelensis.";
RL Appl. Environ. Microbiol. 68:5082-5095(2002).
DR DR EMBL; AL31825; CAD30135.1; -.
KW KW Hypothetical protein.
SQ SEQUENCE 88 AA; 10480 MW; 545BF0363F697398 CRC64;

Query Match          2.5%; Score 7; DB 2; Length 88;

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Best Local Similarity 100.0%; Pred. NO. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLRQLVR 89
Db 19 QLRQLVR 25
|||||

RESULT 20
Q870H0 PRELIMINARY; PRT; 92 AA.
AC Q870H0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sun4p (Fragment).
GN Name=Sun4;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
[1]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=s288c;
RA Zhang Z., Dietrich F.S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY245796; AAP04346.1; -.
FT NON TER 92
SQ SEQUENCE 92 AA; 9444 MW; 6AA4C3BE7C157E67 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 VAVTVYV 37
Db 47 VAVTVYV 53
|||||

RESULT 21
Q9HSN3 PRELIMINARY; PRT; 93 AA.
ID Q9HSN3
AC Q9HSN3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vng0151c.
OS OrderedLocuNames=VNG0151.3, VNG0151C;
GN Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=2050483; PubMed=11016950; DOI=10.1073/pnas.190337797;
RX NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Laaky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Madden D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlshroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
[1]
RN EMBL; AE004981; AAG18770.1; -.
PIR; F84175; F84175.
DR InterPro; IPR011594; Thioredoxin like.
DR ProDom; PD003679; Thioredoxin_like; 1.
KW Complete proteome.
SQ SEQUENCE 93 AA; 9680 MW; AE96B8359F340B49 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 93;

```

Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 FVSVTNE 263
Db 13 FVSVTNE 19
|||||

RESULT 22
Q8PMD7 PRELIMINARY; PRT; 94 AA.
AC Q8PMD7
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Hypothetical protein XAC1492.
GN OrderedLocusNames=XAC1492;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins B.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
DR EMBL; AB011781; AAM36362.1; --
KW Complete proteome.

QY 253 NDRIFVS 259
Db 65 NDRIFVS 71
|||||

RESULT 23
AH4_TOXGO STANDARD; PRT; 96 AA.
AC Q27001;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antigen H4 (Fragment).
GN Names=H4;
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP STRAIN=RH;
RC MEDLINE=91216437; PubMed=2022319; DOI=10.1016/0378-1119(91)90044-C;

Johnson A.M., Illana S.;
"Cloning of Toxoplasma gondii gene fragments encoding diagnostic
antigens.";
RL Gene 99:127-132(1991).

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CC or send an email to license@isb-sib.ch).

DR EMBL; M57302; AAA30139.1; --
DR FIR; PS0423; PS0423.
KW Antigen.
FT NON TER 1 34 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 34 34
SQ SEQUENCE 96 AA; 10853 MW; 69C7C2D14890FA53 CRC64;
Query Match 2.5%; Score 7; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FQEEIKE 198
Db 2 FQEEIKE 8
|||||

RESULT 24
Q9LV97 PRELIMINARY; PRT; 106 AA.
ID Q9LV97
AC Q9LV97
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
DE Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MXK3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:31-63(2000).
DR EMBL; AB019236; BAA97292.1; --
SQ SEQUENCE 106 AA; 12377 MW; A85ECD52EF507B4C CRC64;

Query Match 2.5%; Score 7; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 IVIFTVL 25
Db 17 IVIFTVL 23
|||||

RESULT 25
Q97Y77 PRELIMINARY; PRT; 107 AA.
ID Q97Y77
AC Q97Y77
DT 01-OCT-2001 (T-EMBLrel. 18, Created)
DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein SSO1462.
GN OrderedLocusNames=SSO1462;
OS Sulfolobus solfataricus.

Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
NCBI_TaxID=2287;
[1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RA MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
RX She Q., Singh R.K., Cafaloni F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtiss B.A.,
RA De Moors A., Erasuo G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006762; AAK41690.1; -
DR PIR; C90304; C90304.
DR InterPro; IPR007272; DUF395.
DR Pfam; PF04143; DUF395; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 107 AA; 12018 MW; 9471937E9819A836 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 FFGAFLV 280
DB 46 FFGAFLV 52

RESULT 26
Q932M3 PRELIMINARY; PRT; 112 AA.
ID Q932M3
AC Q932M3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Truncated resolvase.
GN Name=truncated-res; OrderedLocustNames=SNVP030;
GS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OG Plasmid VRSAp.
OX NCBI_TaxID=158878;
ON [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N., Kawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hirakawa H., Kikuchi S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yashima A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003367; BAB47538.1; -
DR HSPB; P03012; 2RSL.
DR GO; GO:000150; F:recombinase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR006118; Recombinase_S.
DR InterPro; IPR006119; resolvase_N.
DR Pfam; PF0239; Resolvase; 1.
DR PROSITE; PS00397; RECOMBINASES_1.
DR PROSITE; PS00398; RECOMBINASES_2; 1.
KW Complete proteome; Plasmid.
SQ SEQUENCE 112 AA; 12884 MW; 1ABB806BBAEDF522 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 92;

P72087; 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE Hemolysin A homolog (Fragment).
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Z2491;
 RX MEDLINE=97008141; PubMed=8855317; DOI=10.1073/pnas.93.20.11109;
 RA Tinsley C.R., Nasif X.;
 RT "Analysis of the genetic differences between *Neisseria meningitidis*
 RT and *Neisseria gonorrhoeae*: two closely related bacteria expressing two
 RT different pathogenicities.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:11109-11114(1996).
 DR EMBL; U56741; AAC44481.1; -.
 FT NON_TER 1 125
 FT NON_TER 125 125
 SQ SEQUENCE 125 AA; 12834 MW; 92D8F57FD493496 CRC64;

 Query Match 2.5%; Score 7; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 123 AAHITGT 129
 Db |||||
 18 AAHITGT 24

 RESULT 30
 Q8MM82
 ID Q8MM82 PRELIMINARY; PRT; 134 AA.
 AC Q8MM82;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Hypothetical protein T02C12.4.
 GN ORFNames=T02C12.4;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode *C.elegans*: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Gardner A.E.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Lloyd C.R.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z35603; CAD36484.1; JOINED.
 DR EMBL; Z38112; CAD36484.1; -.
 DR EMBL; Z35603; CAD36496.1; -.
 DR EMBL; Z38112; CAD36496.1; JOINED.
 DR WormBase; WBGene00011369; T02C12.4.
 DR WormPep; T02C12.4; CE30825.
 KW Hypothetical protein.
 SQ SEQUENCE 134 AA; 15340 MW; 1DB9A0AD8814E477 CRC64;

 Query Match 2.5%; Score 7; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 236 EYGLYSI 242
 Db |||||
 81 EYGLYSI 87

 RESULT 31
 Q9YBC2
 ID Q9YBC2 PRELIMINARY; PRT; 155 AA.
 AC Q9YBC2;
 DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Hypothetical protein APE1675.
 GN OrderedLocusNames=APE1675;
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Maikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anka H., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, *Aeropyrum pernix* K1.";
 RL DNA Res. 6:83-101(1999).
 DR EMBL; AP000062; BAA80676.1; -.
 DR PIR; G72548; G72548.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 155 AA; 16841 MW; 1AA47C685D52939B CRC64;

 Query Match 2.5%; Score 7; DB 2; Length 155;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 135 TLSPNS 141
 Db |||||
 88 TLSPNS 94

 RESULT 32
 Q83TUI
 ID Q83TUI PRELIMINARY; PRT; 157 AA.
 AC Q83TUI;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS *Staphylococcus aureus*.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Newman, and ISP479C;
 RX MEDLINE=22925846; PubMed=14563862;
 RX DOI=10.1128/JB.185.21.6278-6286.2003;
 RA Steinhuber A., Goerke C., Bayer M.G.;
 RT "Molecular architecture of the regulatory locus *sae* of *Staphylococcus*
 RT *aureus* and its impact on the expression of virulence factors.";
 RL J. Bacteriol. 185:6278-6286(2003).
 DR EMBL; AJ556794; CAD89109.1; -.
 DR EMBL; AJ556795; CAD89113.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 157 AA; 17665 MW; AF973D8D9D5D5963E CRC64;

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Query Match      2.5%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 ASFFGAF 278
Db 90 ASFFGAF 96

RESULT 33
Q6GBC3 PRELIMINARY; PRT; 157 AA.
ID Q6GBC3
AC Q6GBC3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative membrane protein.
GN OrderedLocusNames=SAS0672;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG42448.1; -.
KW Complete proteome.
SQ SEQUENCE 157 AA; 17665 MW; AF973D8D95D5963E CRC64;

Query Match      2.5%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 ASFFGAF 278
Db 90 ASFFGAF 96

RESULT 34
Q6GIT5 PRELIMINARY; PRT; 157 AA.
ID Q6GIT5
AC Q6GIT5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative membrane protein.
GN OrderedLocusNames=SAR0760;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;

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RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG39770.1; -.
KW Complete proteome.
SQ SEQUENCE 157 AA; 17665 MW; AF973D8D95D5963E CRC64;

Query Match      2.5%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 ASFFGAF 278
Db 90 ASFFGAF 96

RESULT 35
Q9N8D4 PRELIMINARY; PRT; 172 AA.
ID Q9N8D4
AC Q9N8D4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acetyltransferase, possible.
GN Name=Tb927.1.4490;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU927;
RA Hall N., Berriman M., Lennard N.J., Harris B.R., Hertz-Fowler C.,
RA Bart-Delabesse E.N., Gerrard C.S., Atkin R.J., Barron A.J., Bowman S.,
RA Bray-Allen S.P., Brington F., Clark L.N., Corton C.H., Cronin A.,
RA Davies R., Doggett J., Fraser A., Gruter E., Hall S., Harper A.D.,
RA Kay M.P., Leech V., Mayes R., Price C., Quail M.A., Rabinowitch E.,
RA Reitter C., Rutherford K., Sasse J., Sharp S., Showkeen R.,
RA Macleod A., Taylor S., Tweedie A., Turner C.M.R., Tait A., Gull K.,
RA Barrell B., Melville S.E.;
RT "The DNA sequence of chromosome I of an African trypanosome: gene
RT content, chromosome organisation, recombination and polymorphism.";
RL Nucleic Acids Res. 31:4864-4873(2003).
DR EMBL; AL929607; CAB95609.1; -.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000182; GCNSacetyl_trans.
DR Pfam; PF00583; Acetyltransf_1; I.
KW Transferase.
SQ SEQUENCE 172 AA; 19682 MW; B5DD1A59A77E2AB9 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 NSKNEKA 146
Db 142 NSKNEKA 148

RESULT 36
Q7R3Y3 PRELIMINARY; PRT; 191 AA.
ID Q7R3Y3
AC Q7R3Y3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GUP_69.61978.62553.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;

```

RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAC801000012; EAA42045.1; -;
 SQ SEQUENCE 191 AA; 21255 MW; FID7FEF8FFCC2A73 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 191;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 ELKQWQD 47
 Db 125 ELKQWQD 131
 |||||

RESULT 37
 YQ05_XANCP YQ05_XANCP STANDARD; PRT; 193 AA.
 ID YQ05_XANCP STANDARD; PRT; 193 AA.
 AC Q8P7K6;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DE Hypothetical UPF0307 protein XCC2605.
 GN OrderedLocusNames=XCC2605;
 OS Xanthomonas campestris (pv. campestris).
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 CC Xanthomonadaceae; Xanthomonas.
 CC NCBI_TaxID=340;
 [1]

SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RA "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.";
 RL Nature 417:459-463(2002).

-!- SIMILARITY: Belongs to the UPF0307 family.
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 CC or send an email to license@isb-sib.ch).
 CC SEQUENCE 193 AA; 22001 MW; F00A357929414027 CRC64;

EMBL; AE012372; AAM41877.1; -;
 DR HAMAP; MF 00765; -; 1.
 DR InterPro; IPR006839; DUF615.
 DR InterPro; IPR001232; Skp1.
 DR InterPro; IPR008945; Skp1_Skp2.
 DR Pfam; PF04751; DUF615; 1.
 DR PIRSF; PIRSF016183; UCP016183; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 193 AA; 22001 MW; F00A357929414027 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLQRLVR 89
 Db 138 QLQRLVR 144
 |||||

Query Match 2.5%; Score 7; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLQRLVR 89
 Db 138 QLQRLVR 144
 |||||

RESULT 38
 YR66_XANAC YR66_XANAC STANDARD; PRT; 193 AA.
 ID YR66_XANAC STANDARD; PRT; 193 AA.
 AC Q8PIK3;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DE Hypothetical UPF0307 protein XAC2766.
 GN OrderedLocusNames=XAC2766;
 OS Xanthomonas axonopodis (pv. citri).
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 CC Xanthomonadaceae; Xanthomonas.
 CC NCBI_TaxID=92829;
 [1]

SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RA "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.";
 RL Nature 417:459-463(2002).

-!- SIMILARITY: Belongs to the UPF0307 family.
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 CC or send an email to license@isb-sib.ch).
 CC SEQUENCE 193 AA; 22033 MW; F3418B2APAF98257 CRC64;

EMBL; AE011917; AAM37611.1; ALT_INIT.
 DR HAMAP; MF 00765; -; 1.
 DR InterPro; IPR006839; DUF615.
 DR InterPro; IPR001232; Skp1.
 DR InterPro; IPR008945; Skp1_Skp2.
 DR Pfam; PF04751; DUF615; 1.
 DR PIRSF; PIRSF016183; UCP016183; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 193 AA; 22033 MW; F3418B2APAF98257 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLQRLVR 89
 Db 138 QLQRLVR 144
 |||||

```

RESULT 39
LIPB NITEU STANDARD; PRT; 204 AA.
AC Q82UJ6; 2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-MAR-2004 (Rel. 45, Last annotation update)
DE Lipoyltransferase [EC 2.3.1.-] (Lipoyl-(acyl-carrier protein)-protein
DE -N-lipoyltransferase) (Lipoate-protein ligase B).
GN Name=lipB; OrderedLocusNames=NEI148;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IF0 14298;
RX MEDLINE=22586410; PubMed=12700255;
RX DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer P.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Acierio D.M., Holmes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
CC -!- FUNCTION: Catalyzes the transfer of the endogenously synthesized
CC lipate to apoproteins, creating an amide linkage that joins the
CC free carboxyl group of lipate to the epsilon-amino group of a
CC specific lysine residue in lipate-dependent enzymes. Utilizes
CC lipoyl-acyl-carrier protein as a source of lipoyl groups, although
CC octanoyl groups from octanoyl-ACP can also be transferred to the
CC lipoyl domain of apoproteins (By similarity).
CC -!- CATALYTIC ACTIVITY: lipoyl-(acyl-carrier protein) + apo-protein =
CC holo-protein + acyl-carrier protein.
CC -!- PATHWAY: Endogenous lipate metabolism; lipoylation step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the lipB family.
CC -----
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CC -----
DR EMBL; BX321861; CAD85399.1; -.
DR HAMAP; MF_00013; -.
DR InterPro; IPR004143; BPL_LipA_LipB.
DR InterPro; IPR000544; Lipoate_B.
DR Pfam; PF03099; BPL_LipA_LipB_1.
DR ProDom; PD006086; Lipoate_B_1.
DR TIGRFAMs; TIGR00214; lipB; 1.
DR PROSITE; PS01313; lipB; 1.
DR Acyltransferase; Complete proteome; Transferase.
KW ACYLTRANSFERASE; 204 AA; 22764 MW; A83FGEF5F0346E61 CRC64;
SQ SEQUENCE 204 AA; 22764 MW; A83FGEF5F0346E61 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 RQLVRKM 91
Db |||||
97 RQLVRKM 103

RESULT 40
GEMI HUMAN STANDARD; PRT; 209 AA.
ID -GEMI_HUMAN
AC Q75436; Q9H121;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT

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DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Geminin.
GN Name=GMN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98297356; PubMed=9635433; DOI=10.1016/S0092-8674(00)81209-X;
RA McGarry T.J., Kirschner M.W.;
RT "Geminin, an inhibitor of DNA replication, is degraded during
RT mitosis.";
RL Cell 93:1043-1053(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Corby N.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RT TISSUE=Lung, and Urinary bladder;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Inhibits DNA replication by preventing the incorporation
CC of MCM complex into prereplicative complex (pre-RC). It is
CC degraded during the mitotic phase of the cell cycle. Its
CC destruction at the metaphase-anaphase transition permits
CC replication in the succeeding cell cycle.
CC -!- DEVELOPMENTAL STAGE: Absent during G1 phase, accumulates during S,
CC G2, and M phases, and disappears at the time of the metaphase-
CC anaphase transition.
CC -!- SIMILARITY: Belongs to the geminin family.
CC -----
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CC -----
DR EMBL; AF067855; AAC39787.1; -.
DR EMBL; AL133264; CAC21511.1; ALT_INIT.
DR EMBL; BC005185; AAH05185.1; -.
DR EMBL; BC005389; AAH05389.1; -.
DR IntAct; Q75496; -.
DR Genew; HGNC:17493; GMN.
DR H-InvDB; HIX0005629; -.
DR Reactome; O75496; -.
DR GO; GO:0007050; P:cell cycle arrest; TAS.
DR GO; GO:0008156; P:negative regulation of DNA replication; TAS.
DR InterPro; IPR009984; Geminin.
DR Pfam; PF07412; Geminin; 1.
KW Cell cycle.

```

SQ SEQUENCE 209 AA; 23565 MW; 0BAB60F6F5AC252 CRC64;
Query Match 2.5%; Score 7; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 193 QEEIKEN 199
DB 9 QEEIKEN 15
RESULT 41
Q9LTD0 PRELIMINARY; PRT; 217 AA.
ID Q9LTD0
AC Q9LTD0
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE HR-like lesion-inducing protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025608; BAA95731.1; -;
DR InterPro; IPR008637; HR lesion.
DR InterPro; IPR011592; Surf4 rel.
PFam; PF05514; HR lesion; 1.
DR ProDom; PD010195; Surf4 rel. 1.
SQ SEQUENCE 217 AA; 25219 MW; F88CDE1A0BEABC4F CRC64;
Query Match 2.5%; Score 7; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 273 SFFGAF 279
DB 88 SFFGAF 94
RESULT 42
Q6S8A0 PRELIMINARY; PRT; 220 AA.
ID Q6S8A0
AC Q6S8A0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE PIB-type ATPase (Fragment).
OS Acidovorax sp. B0447.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Acidovorax.
OX NCBI_TaxID=263568;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B0447;
RX PubMed=15006795; DOI=10.1128/AEM.70.3.1698-1707.2004;
RA Combs J.M., Barkay T.;
RT "Molecular evidence for the evolution of metal homeostasis genes by
RT lateral gene transfer in bacteria from the deep terrestrial
RT subsurface.";
RA Appl. Environ. Microbiol. 70:1698-1707(2004).

DR EMBL; AY463186; AAS19962.1; -;
DR InterPro; IPR001757; ATPase_EI-E2.
DR InterPro; IPR005834; Dehal_like_Hydro.
PFam; PF00702; Hydrolase; 1.
DR PROSITE; PS00154; ATPASE_EI_E2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 220 220
SQ SEQUENCE 220 AA; 23104 MW; 45AC3A0F411769FE CRC64;
Query Match 2.5%; Score 7; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 173 ELVIHEK 179
DB 126 ELVIHEK 132
RESULT 43
Q89V44 PRELIMINARY; PRT; 220 AA.
ID Q89V44
AC Q89V44;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Brl214 protein.
GN OrderedLocusNames=blr1214;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idegawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005939; BAC46479.1; -;
KW Complete proteome.
SQ SEQUENCE 220 AA; 23332 MW; 0AD03221F4C1A350 CRC64;
Query Match 2.5%; Score 7; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 LVREGRP 119
DB 110 LVREGRP 116
RESULT 44
Q7MMP6 PRELIMINARY; PRT; 222 AA.
ID Q7MMP6
AC Q7MMP6;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein VV1021.
GN OrderedLocusNames=VV1021;
OS Vibrio vulnificus (strain VJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,

RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
 RT "Comparative genome analysis of *Vibrio vulnificus*, a marine
 pathogen."
 RL Genome Res. 13:2577-2587(2003).
 DR EMBL: AP005334; BAC93785.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 222 AA; 24807 MW; 94A0BF9F43F33FAD CRC64;

Query Match 2.5%; Score 7; DB 2; Length 222;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GIFEKE 252
 |||||
 Db 190 GIFEKE 196

RESULT 45

ID Q8DFN8 PRELIMINARY; PRT; 222 AA.
 AC Q8DFN8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Uncharacterized protein conserved in bacteria.
 GN OrderedLocusNames=V10168;
 OS *Vibrio vulnificus*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; *Vibrio*.
 OX NCBI_TaxID=672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6."
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE016797; AAC08706.1; -;
 KW Complete proteome.
 SQ SEQUENCE 222 AA; 24807 MW; 94A0BF9F43F33FAD CRC64;

Query Match 2.5%; Score 7; DB 2; Length 222;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GIFEKE 252
 |||||
 Db 190 GIFEKE 196

RESULT 46

ID Q72XY8 PRELIMINARY; PRT; 230 AA.
 AC Q72XY8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Membrane protein, putative.
 GN OrderedLocusNames=BCES5335.
 OS *Bacillus cereus* (strain ATCC 10987).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=222523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=14960714; DOI=10.1093/nar/gkh258;
 RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
 RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
 RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
 RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic
 adaptations and a large plasmid related to *Bacillus anthracis* pX01."
 RL Nucleic Acids Res. 32:977-988(2004).
 DR EMBL: AE017280; AAS44136.1; -;
 DR TIGR: BCE5235; -;

DR GO: 0016020; C.membrane; IEA.
 DR InterPro: IPR007300; LrgB.
 DR Pfam: PF04172; LrgB; 1.
 KW Complete proteome.
 SQ SEQUENCE 230 AA; 24443 MW; 189C4651DAE35A72 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 VIETVLL 26
 |||||
 Db 11 VIETVLL 17

RESULT 47

ID P90611 PRELIMINARY; PRT; 231 AA.
 AC P90611;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE H4 protein.
 DE Toxoplasma gondii.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
 OC Toxoplasma.
 OX NCBI_TaxID=5811;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BK;
 RX MEDLINE=20542029; PubMed=11087916; DOI=10.1016/S0166-6851(00)00296-6;
 RA Brydges S.D., Sherman G.D., Nockemann S., Loyens A., Daubener W.,
 RA Dubremetz J.F., Curruhera V.B.;
 RT "Molecular characterization of TgMIC5, a proteolytically processed
 antigen secreted from the micronemes of *Toxoplasma gondii*."
 RL Mol. Biochem. Parasitol. 111:51-66(2000).
 DR EMBL: Y09782; CAA70921.1; -;
 SQ SEQUENCE 231 AA; 25984 MW; 9C5B0B4690B36314 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 231;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 192 FQBEIKE 198
 |||||
 Db 137 FQBEIKE 143

RESULT 48

ID Q7PY53 PRELIMINARY; PRT; 232 AA.
 AC Q7PY53;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE AGCP12066.
 GN Names=agCG47164; ORFNames=ENSANGG00000006384;
 OS *Anopheles gambiae* str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; *Anopheles*.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAA0100987; EAA01660.1; -;
 SQ SEQUENCE 232 AA; 25104 MW; C0C96A97FB332E0B CRC64;

Query Match 2.5%; Score 7; DB 2; Length 232;

Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 TVLQSL 29
Db 46 TVLQSL 52

RESULT 49

Q58B3 PRELIMINARY; PRT; 232 AA.

AC Q6S8B3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE P1B-type ATPase (fragment).
OS Acidovorax sp. B0054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Acidovorax.
OX NCBI_TaxID=263555;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B0054;
RX PubMed=15006795; DOI=10.1128/AEM.70.3.1698-1707.2004;
RA Coombs J.M., Barkay T.;
RT "Molecular evidence for the evolution of metal homeostasis genes by lateral gene transfer in bacteria from the deep terrestrial subsurface.";
RL Appl. Environ. Microbiol. 70:1698-1707(2004).
DR EMBL; AY463173; AAS19949.1; -;
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 232
SQ SEQUENCE 232 AA; 24249 MW; F85D924477FB916F CRC64;

Query Match 2.5%; Score 7; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 ELVIHEK 179
Db 139 ELVIHEK 145

RESULT 50

CD7_HUMAN
ID - CD7_HUMAN
AC P09564;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T-cell antigen CD7 precursor (GP40) (T-cell leukemia antigen) (TP41) (Leu-9).
GN Name=CD7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88111517; PubMed=3501369;
RA Aruffo A., Seed B.;
RT "Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS cell expression system.";
RL EMBO J. 6:3313-3316(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91110576; PubMed=1703303;

RA Schanberg L.E., Fleenor D.E., Kurtzberg J., Haynes B.F., Kaufman R.E.;
RT "Isolation and characterization of the genomic human CD7 gene: structural similarity with the murine Thy-1 gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:603-607(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 205-240 FROM N.A.
RX MEDLINE=91267564; PubMed=1711009;
RA Yoshikawa K., Seto M., Ueda R., Obata Y., Notake K., Yokochi T.,
RA Takahashi T.;
RT "Molecular cloning of the gene coding for the human T cell differentiation antigen CD7.";
RL Immunogenetics 33:352-360(1991).
RN [5]
RP TOPOLOGY.
RX MEDLINE=90063052; PubMed=2479685;
RA Ware R.E., Searce R.M., Dietz M.A., Starmer C.F., Palker T.J.,
RA Haynes B.F.;
RT "Characterization of the surface topography and putative tertiary structure of the human CD7 molecule.";
RL J. Immunol. 143:3632-3640(1989).
RN [6]
RP INTERACTION WITH SECTM1.
RX MEDLINE=20119303; PubMed=10652336; DOI=10.1074/jbc.275.5.3431;
RA Lyman S.D., Escobar S., Rousseau A.-M., Armetrong A., Fanslow W.C.;
RT "Identification of CD7 as a cognate of the human K12 (SECTM1) protein.";
RL J. Biol. Chem. 275:3431-3437(2000).
CC -!- FUNCTION: Not yet known.
CC -!- SUBUNIT: Interacts with SECTM1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD7 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd7.htm".
CC
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CC
CC EMBL; X06180; CAA29546.1; -;
CC EMBL; M37271; AAA51953.1; -;
CC EMBL; BC009293; AAH09293.1; -;
CC EMBL; BC013297; AAH13297.1; -;
CC EMBL; D00749; BAA00646.1; -;
CC EMBL; D00747; BAA00646.1; JOINED.
CC EMBL; D00748; BAA00646.1; JOINED.

```
DR PIR; A39016; A39016.
DR HSSP; P01607; 1BW.
DR Genew; HGNC:1695; CD7.
DR H-InvDB; HIX0014252; -.
DR MIM; 186820; -.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR GO; GO:0005624; C: membrane fraction; TAS.
DR GO; GO:0005886; C: plasma membrane; TAS.
DR GO; GO:0004872; F: receptor activity; TAS.
DR GO; GO:0006955; P: immune response; TAS.
DR GO; GO:0042110; P: T-cell activation; TAS.
DR GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. .; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Antigen; Glycoprotein; Immune response; Immunoglobulin domain;
KW Lipoprotein; Palmitate; Receptor; Repeat; Signal; T-cell;
KW Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 240 T-cell antigen CD7.
FT DOMAIN 26 180 Extracellular (Probable).
FT TRANSMEM 181 201 Probable.
FT DOMAIN 202 240 Cytoplasmic (Probable).
FT DOMAIN 26 130 Ig-like.
FT DOMAIN 145 180 4 X 9 AA tandem repeats, potential spacer
function.
FT DISULFID 35 142 Potential.
FT DISULFID 48 114 Potential.
FT LIPID 198 198 S-palmitoyl cysteine.
FT CARBOHYD 45 45 N-linked (GlcNAc. .).
FT CARBOHYD 96 96 N-linked (GlcNAc. .).
FT REPEAT 145 153 1.
FT REPEAT 154 162 2.
FT REPEAT 163 171 3.
FT REPEAT 172 180 4.
FT REPEAT 172 180 4.
SQ SEQUENCE 240 AA; 25409 MW; EBBCE08279552108 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 134 NTLSPN 140
Db 231 NTLSPN 237

RESULT 51
O64MD3 PRELIMINARY; PRT; 240 AA.
AC O64MD3
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=BFP0027;
OS Bacteroides fragilis.
OC Bacterioidetes; Bacteroides (class); Bacteroidales;
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR EMBL; AP006842; BAD51354.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 240 AA; 27646 MW; DC1CF4292674BEF8 CRC64;
```

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Query Match 2.5%; Score 7; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 255 RIFVSVT 261
Db 91 RIFVSVT 97

RESULT 53
O99RD5 PRELIMINARY; PRT; 247 AA.
AC O99RD5
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Staphylococcus aureus (strain Mu50 / ATCC 700699).
GN Name=sarH2; OrderedLocustNames=SAV2499;
OS Staphylococcus aureus
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
EX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003365; BAB58661.1; -.
DR PIR; D90053; D90053.
DR HSSP; Q53777; 1FZP.
DR InterPro; IPR010166; Staph reg Sar.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
```

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Query Match 2.5%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 255 RIFVSVT 261
Db 91 RIFVSVT 97

RESULT 53
O99RD5 PRELIMINARY; PRT; 247 AA.
AC O99RD5
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Staphylococcus aureus (strain Mu50 / ATCC 700699).
GN Name=sarH2; OrderedLocustNames=SAV2499;
OS Staphylococcus aureus
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RC MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
EX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003365; BAB58661.1; -.
DR PIR; D90053; D90053.
DR HSSP; Q53777; 1FZP.
DR InterPro; IPR010166; Staph reg Sar.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
```



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DR TIGRFAMs; TIGR01889; Staph_reg_Sar; 2.
KW Complete proteome.
SQ SEQUENCE 247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 247;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
DB 91 RIFVSVT 97

RESULT 54
Q7A004 PRELIMINARY; PRT; 247 AA.
AC Q7A004;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE SarH2 protein.
GN Name=sarH2; OrderedLocusNames=MW2418;
OS Staphylococcus aureus (strain MW2)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004830; BAB96283.1; -.
DR InterPro; IPR010166; Staph_reg_Sar.
DR TIGRFAMs; TIGR01889; Staph_reg_Sar; 2.
KW Complete proteome.
SQ SEQUENCE 247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 247;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
DB 91 RIFVSVT 97

RESULT 55
Q7A3K0 PRELIMINARY; PRT; 247 AA.
AC Q7A3K0;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE SarH2 protein.
GN Name=sarH2; OrderedLocusNames=SA2287;
OS Staphylococcus aureus (strain N315)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003137; BAB43590.1; -.
DR InterPro; IPR010166; Staph_reg_Sar.
DR TIGRFAMs; TIGR01889; Staph_reg_Sar; 2.
KW Complete proteome.
SQ SEQUENCE 247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 247;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
DB 91 RIFVSVT 97

RESULT 56
Q6G6H6 PRELIMINARY; PRT; 247 AA.
AC Q6G6H6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Putative staphylococcal accessory regulator.
GN OrderedLocusNames=SA2385;
OS Staphylococcus aureus (strain MSSA476)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.040251101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG44199.1; -.
DR InterPro; IPR010166; Staph_reg_Sar.
DR TIGRFAMs; TIGR01889; Staph_reg_Sar; 2.
KW Complete proteome.
SQ SEQUENCE 247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 247;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
DB 91 RIFVSVT 97

RESULT 57
O94262 PRELIMINARY; PRT; 251 AA.
AC O94262;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE SPBP87.13 protein.
GN Name=SPBP87.13;
OS Schizosaccharomyces pombe (Fission yeast)
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;

```

Schizosaccharomyces.

OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RX MEDLINE=218448401; PubMed=11859360; DOI=10.1038/nature724;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,
 RA Gabel C., Fuchs M., Dusterhoft A., Fritzc C., Holzer E., Moestl D.,
 RA Hilbert H., Borzym K., Langer I., Beck A., Leirach H., Reinhardt R.,
 RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 DR EMBL; AL032684; CAA21798.1; -;
 DR PIR; T40807; T40807;
 DR GeneDB Spombe; SPBP887.l3; -;
 SQ SEQUENCE 251 AA; 27746 MW; CG31E344FDC0D686 CRC64;

 Query Match 2.5%; Score 7; DB 2; Length 251;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 66 DPNDDES 72
 Db 73 DPNDDES 79

 RESULT 58
 Q98D64 PRELIMINARY; PRT; 253 AA.
 AC Q98D64;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE M14839 protein.
 OS Rhizobium loti (Mesorhizobium loti).
 GN OrderedLocusNames=m14839;
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Yamakawa S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti".
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003005; BAB51407.1; -;
 DR InterPro; IPR000160; GGDEF.

DR Pfam; PF00990; GGDEF; 1.
 DR SMART; SMO0267; DUFL; 1.
 DR TIGRFAMs; TIGR00254; GGDEF; 1.
 DR PROSITE; PSS0887; GGDEF; 1.
 SQ Complete proteome.
 KW SEQUENCE 253 AA; 27656 MW; 358A4F06B9B6C8E CRC64;

 Query Match 2.5%; Score 7; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 275 FGAFVLVG 281
 Db 168 FGAFVLVG 174

 RESULT 59
 Q636T1 PRELIMINARY; PRT; 271 AA.
 AC Q636T1;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hydrolase, alpha/beta fold family (EC 3.7.1.-).
 GN ORFNames=BTZK3504;
 OS Bacillus cereus ZK.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=288681;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZK;
 RA Brettn T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H., Tice H., Tice H., Tice H.,
 RT "Complete genome sequence of Bacillus cereus ZK.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CP000001; AAU16762.1; -;
 KW Hydrolase.
 SQ SEQUENCE 271 AA; 31281 MW; 85C92D54129184BE CRC64;

 Query Match 2.5%; Score 7; DB 2; Length 271;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 191 RFQEEIK 197
 Db 170 RFQEEIK 176

 RESULT 60
 Q81WU0 PRELIMINARY; PRT; 271 AA.
 AC Q81WU0; Q6HU23; Q6KP68;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hydrolase, alpha/beta fold family.
 GN OrderedLocusNames=BA3877, BA3592, GBAA3877;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1392;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Anes / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
 RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.D., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,

RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Kohler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of *Bacillus anthracis* Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AR017036; AAP27611.1; -;
DR EMBL; AR017334; AAT32991.1; -;
DR EMBL; AR017225; AAT55696.1; -;
DR TIGR; BA3877; -;
DR TIGR; GBA3877; -;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR003089; AB_Hydrolase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00561; Abhydrolase_1; i.
DR PRINTS; PR00111; ABHYDROLASE.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 271 AA; 31338 MW; D01B8F4D025FF187 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 191 RFQEEIK 197
Db 170 RFQEEIK 176
|||||

RESULT 61
ID Q6HF64 PRELIMINARY; PRT; 271 AA.
AC Q6HF64;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hydrolase, alpha/beta fold family (EC 3.7.1.-).
GN OrderedLocusNames=BT927_3492;
OS *Bacillus thuringiensis* (subsp. konkukian).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of *Bacillus thuringiensis* 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AR017355; AAT60562.1; -;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR003089; AB_Hydrolase.
DR Pfam; PF00561; Abhydrolase_1; i.
DR PRINTS; PR00111; ABHYDROLASE.

KW Complete proteome.
SQ SEQUENCE 271 AA; 31382 MW; 8E6769086609B7F3 CRC64;
Query Match 2.5%; Score 7; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 191 RFQEEIK 197
Db 170 RFQEEIK 176
|||||

RESULT 62
ID Q8ROLO PRELIMINARY; PRT; 293 AA.
AC Q8ROLO;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BC026645 protein (fragment).
GN Name=BC026645;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026645; AAH26645.1; -;
DR MGD; MGI:2446129; BC026645.
FT NON_TER 1
SQ SEQUENCE 293 AA; 33723 MW; 642B913C78884195 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 93 LRTSEET 99
Db 5 LRTSEET 11
|||||

RESULT 63
LGT_CHLCV
ID LGT_CHLCV STANDARD; PRT; 296 AA.
AC Q823E7;
DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DE 25-OCT-2004 (Rel. 45, Last annotation update)
 GN Name=lgf; OrderedLocusNames=CCA00471;
 OS Chlamydomophila caviae.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
 OX NCBI_TaxID=83557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPIC;
 RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
 RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
 RA Heidelberg J.F., Holtzapple E.K., Khouri H.M., Fedorova N.B.,
 RA Carty H.A., Unayam L.A., Haft D.H., Peterson J.D., Beanan M.J.,
 RA White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G.,
 RA Bavoil P.M., Fraser C.M.;
 RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
 examining the role of niche-specific genes in the evolution of the
 Chlamydiaceae.";
 RL Nucleic Acids Res. 31:2134-2147(2003).
 CC -!- FUNCTION: Transfers the N-acyl diglyceride group on what will
 become the N-terminal cysteine of membrane lipoproteins (by
 similarity).
 CC -!- PATHWAY: Lipoprotein biosynthesis; first step.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 (Probable).
 CC -!- SIMILARITY: Belongs to the lgt family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AEO16995; AAP05216.1; -;
 DR TIGR; CCA00471; -;
 DR HAMAP; MF 01147; -; 1.
 DR InterPro; IPR001640; LGT.
 DR Pfam; PF01790; LGT; 1.
 DR TIGRFAMs; TIGR00544; lgt; 1.
 DR PROSITE; PS01311; LGT; FALSE NEG.
 KW Complete proteome; Inner membrane; Transferase; Transmembrane.
 FT TRANSMEM 26 48 Potential.
 FT TRANSMEM 69 91 Potential.
 FT TRANSMEM 111 130 Potential.
 FT TRANSMEM 137 159 Potential.
 FT TRANSMEM 194 216 Potential.
 FT TRANSMEM 223 245 Potential.
 FT TRANSMEM 260 282 Potential.
 SQ SEQUENCE 296 AA; 33457 MW; 1E148CA397939B64 CRC64;
 Query Match 2.5%; Score 7; DB 1; Length 296;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 53 GIACFLK 59
 Db 278 GIACFLK 284
 RESULT 64
 Q8DXW4 PRELIMINARY; PRT; 298 AA.
 AC Q8DXW4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Membrane protein, putative.
 GN OrderedLocusNames=SAG1731;
 OS Streptococcus agalactiae (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.
 OX NCBI_TaxID=216466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
 RA Tettelin H., Masiognani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
 RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
 RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 emerging human pathogen, serotype V Streptococcus agalactiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
 DR EMBL; AEO14270; AAN00594.1; -;
 DR TIGR; SAG1731; -;
 KW Complete proteome.
 SQ SEQUENCE 298 AA; 32410 MW; EAF7720189133FDE CRC64;
 Query Match 2.5%; Score 7; DB 2; Length 298;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 VLLQSLC 30
 Db 92 VLLQSLC 98
 RESULT 65
 Q8E3I3 PRELIMINARY; PRT; 298 AA.
 AC Q8E3I3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein gbs1776.
 GN OrderedLocusNames=gbs1776;
 OS Streptococcus agalactiae (serotype III).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216495;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEM316 / Serotype III;
 RX MEDLINE=2242508; PubMed=12354221;
 RA Glaeser P., Ruñiok C., Buchrieser C., Chevalier F., Frangeul L.,
 RA Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
 RA Kunst F.;
 RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
 invasive neonatal disease.";
 RL Mol. Microbiol. 45:1499-1513(2002).
 DR EMBL; AL766853; CAD47435.1; -;
 DR SAGList; gbs1776; -;
 KW Complete proteome.
 SQ SEQUENCE 298 AA; 32452 MW; 5BF7720198133368 CRC64;
 Query Match 2.5%; Score 7; DB 2; Length 298;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 VLLQSLC 30
 Db 92 VLLQSLC 98
 RESULT 66
 Q6KZP1 PRELIMINARY; PRT; 305 AA.
 AC Q6KZP1;

05-JUL-2004 (TrEMBLrel. 27, Created)
 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Glucose/mannose-6-phosphate isomerase (EC 5.3.1.9).
 GN OrderedLocusNames=PT01226;
 OS Picrophilus torridus.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 OC Picrophilaceae; Picrophilus.
 OX NCBI_TaxID=82076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 9790 / ATCC 700027;
 RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
 RA Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
 RA Schepers B., Dock C., Antranikian G., Liebl W.;
 RT "Genome sequence of Picrophilus torridus and its implications for life
 RT around pH 0."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
 DR EMBL: AE017261; AAT43811.1; -.
 DR GO: GO:0004347; F:glucose-6-phosphate isomerase activity; IEA.
 DR GO: GO:0016853; F:isomerase activity; IEA.
 DR GO: GO:0005529; F:sugar binding; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR001347; SIS.
 DR Pfam: PF01380; SIS: 1.
 KW Complete proteome; Isomerase.
 SQ SEQUENCE 305 AA; 35516 MW; 405D8A6001AC86CB CRC64;
 Query Match 2.5%; Score 7; DB 2; Length 305;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 EETISTV 103
 DB 81 EETISTV 87
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 RESULT 67
 Q626A7 PRELIMINARY; PRT; 314 AA.
 ID Q626A7
 AC Q626A7
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative annexin P35.
 GN Names=P0627E03.4; Synonyms=OJ1288 G09.26;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the annexin family.
 DR EMBL: AP005012; BADI7230.1; -.
 DR EMBL: AP004119; BADI5571.1; -.
 DR HSP; P12429; IAXN.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR GO: GO:0005544; F:calcium-dependent phospholipid binding; IEA.
 DR InterPro: IPR001464; Annexin.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin. 4.
 DR SMART: SM00335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 1.
 KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
 KW Repeat.
 SQ SEQUENCE 314 AA; 35554 MW; 1BF535BDBFD4AF2 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 122 VAAHITG 128
 DB 137 VAAHITG 143
 |||||
 RESULT 68
 Q96QL7 PRELIMINARY; PRT; 318 AA.
 ID Q96QL7
 AC Q96QL7
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CREB1 protein (CAMP responsive element binding protein-like 1).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skolala U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC008394; AAH08394.1; -.
 DR EMBL: BT007042; AAP35691.1; -.
 SQ SEQUENCE 318 AA; 33894 MW; D70E20D5409C165B CRC64;
 Query Match 2.5%; Score 7; DB 2; Length 318;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 TVLLQSL 29
 DB 266 TVLLQSL 272
 |||||
 RESULT 69
 Q9VI33 PRELIMINARY; PRT; 322 AA.
 ID Q9VI33

AC Q9VI133;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Q92336-PA (AT025555p).
GN ORFNames=CG2336;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier A.S., Fleischmann W.,
RA Fessler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclele J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Stimpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J., Ye J.,
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paclele J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers S.E., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun. Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a Genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mirra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.B., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Paclele J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003674; AAF54111.4; -;
DR EMBL; AY089235; AAL89973.1; -;
DR InCont; Q9V133; -;
DR FlyBase; FBGN0037455; CG2336.
DR InterPro; IPR009961; DUF1487.
DR Pfam; PF07368; DUF1487; 1.
SQ SEQUENCE 322 AA; 36891 MW; D8680A7AC3BB5988 CRC64;
Query Match 2.5%; Score 7; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 207 VOYIYKY 213
Db 16 VOYIYKY 22
RESULT 70
Q9PEN6 PRELIMINARY; PRT; 327 AA.
AC Q9PEN6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=Xf0992;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=23717;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Aruda P., Abreu F.A., Acencio M.,
RA Alvares R., Alves L.M.C., Araya J.E., Bata G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

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RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kramar E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.P.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Maidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR ENBL; AE003937; AAF83802.1; -.
DR PIR; H82736; H82736.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR000379; Ser esters.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 327 AA; 35553 MW; 96A5841EB1A08E90 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117
DB 164 SPLVRER 170

RESULT 71
Q9ZKY9 ID Q9ZKY9 PRELIMINARY; PRT; 329 AA.
AC Q9ZKY9
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ADP-L-GLYCERO-D-MANNHEPTOSE-6-EPIMERASE.
GN Name-gmhd; OrderedLocNames=JHP0793;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR ENBL; AE001509; AAD06369.1; -.
DR PIR; D71887; D71887.
DR HSSP; P14169; IORR.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0009225; P:nucleotide-sugar metabolism; IEA.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
KW Complete proteome.
SQ SEQUENCE 329 AA; 37351 MW; DD1003F6A8C7A720 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117
DB 164 SPLVRER 170

RESULT 72
Q7VJZ3 ID Q7VJZ3 PRELIMINARY; PRT; 343 AA.
AC Q7VJZ3
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DTPD-D-glucose 4,6-dehydratase (EC 4.2.1.46).
GN OrderedLocNames=HH0099;
OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=32025;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 51449 / 3B1;
RX MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
RA Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
RA Bell M., Droege M., Partmann B., Fischer H.-P., Ge Z., Hoerster A.,
RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
RT "The complete genome sequence of the carcinogenic bacterium
RT Helicobacter hepaticus.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
CC -!- SIMILARITY: Belongs to the sugar epimerase family.
DR ENBL; AE017144; AAP76696.1; -.
DR HSSP; P27830; IBXK.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008460; F:DTPD-glucose 4,6-dehydratase activity; IEA.
DR GO; GO:0009225; P:nucleotide-sugar metabolism; IEA.
DR InterPro; IPR005888; dTDP gluc dehyd.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
DR TIGRFAMs; TIGR01181; dTDP gluc dehyd; 1.
KW Complete proteome; NAD.
SQ SEQUENCE 343 AA; 38920 MW; B528F6F2710A40D2 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 YIYKTS 215
DB 329 YIYKTS 335

RESULT 73
O84846 ID O84846 PRELIMINARY; PRT; 354 AA.
AC O84846
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CT839.
GN OrderedLocNames=CT839;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=D / UW-3 / Cx;
RX MEDLINE=99000809; PubMed=97841136; DOI=10.1126/science.282.5389.754;
RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).

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DR EMBL; AE001356; AAC68436.1; -.
DR PIR; G71465; G71465.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR005495; Yjgp_YjgQ.
DR Pfam; PF03739; Yjgp_YjgQ; 1.
KW Complete proteome.
SQ SEQUENCE 354 AA; 40065 MW; AD79C8F2CD59F4E5 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
Db 150 KENDRIF 156
|||||

RESULT 74
Q9PL80 PRELIMINARY; PRT; 354 AA.
AC Q9PL80;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Hypothetical protein TC0227.
DE Hypothetical protein TC0227.
GN OrderedLocusNames=TC0227;
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
ON NCBI_TaxID=83560;
RX SEQUENCE FROM N.A.
RC STRAIN=Mopn / Nigg;
RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE002289; AAF39099.1; -.
DR PIR; A81728; A81728.
DR TIGR; TC0227; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR005495; Yjgp_YjgQ.
DR Pfam; PF03739; Yjgp_YjgQ; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 354 AA; 40145 MW; E6A1317A124C10D1 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
Db 150 KENDRIF 156
|||||

RESULT 75
Q9AVE6 PRELIMINARY; PRT; 359 AA.
AC Q9AVE6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE OStATC protein.
GN Names=OStATC; Synonyms=B1080D07.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
ON NCBI_TaxID=39947;

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RN SEQUENCE FROM N.A.
RP MEDLINE=21140310; PubMed=11244106; DOI=10.1104/pp.125.3.1248;
RX Agrawal G.K., Yamazaki M., Kobayashi M., Hirochika R., Miyao A.,
RA Hirochika H.;
RT "Screening of the rice viviparous mutants generated by endogenous
RT retrotransposon Tos17 insertion. Tagging of a zeaxanthin epoxidase
RT gene and a novel ostaric gene."
RL Plant Physiol. 125:1248-1257(2001).
RN [2]
SQ SEQUENCE FROM N.A.
RP PubMed=12447438; DOI=10.1038/nature01184;
RX Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakaashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K. Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1."
RL Nature 420:312-316(2002).
DR EMBL; AB050885; BAB39766.1; -.
DR EMBL; AP003203; BAB64068.1; -.
DR Gramene; Q9AVE6; -.
DR InterPro; IPR002033; Translocase.
DR Pfam; PF0902; TatC; 1.
DR PRINTS; PR01840; TATCFAMILY.
DR TIGRPFAM; TIGR00945; tatC; 1.
DR PROSITE; PS01218; TATC; 1.
SQ SEQUENCE 359 AA; 38763 MW; D25349B32FE1B540 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 DRIFSV 260
Db 141 DRIFSV 147
|||||

Search completed: June 22, 2005, 06:51:54
Job time : 183 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:03:21 ; Search time 164 Seconds
(without alignments)
662.681 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MAMVEQGPGSLGTCVTLIV.....NEHLIDMDHEASFFGAFVLG 281

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980a:*

2: Geneseqp1990a:*

3: Geneseqp2000a:*

4: Geneseqp2001a:*

5: Geneseqp2002a:*

6: Geneseqp2003a:*

7: Geneseqp2003bs:*

8: Geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	281	100.0	281	2	AAW19777	Aaw19777 Novel cyt
2	281	100.0	281	2	AAW27134	Aaw27134 Human Apo
3	281	100.0	281	2	AAW19787	Aaw19787 Human apo
4	281	100.0	281	2	AAW76829	Aaw76829 Human TL2
5	281	100.0	281	2	AAW56760	Aaw56760 Human TRA
6	281	100.0	281	2	AAW44354	Aaw44354 Human AGP
7	281	100.0	281	2	AAW01517	Aaw01517 Protein a
8	281	100.0	281	2	AAW27012	Aaw27012 Human Apo
9	281	100.0	281	3	AAW81956	Aaw81956 Human Apo
10	281	100.0	281	3	AAW24038	Aaw24038 Human PRO
11	281	100.0	281	3	AAW08545	Aaw08545 Amino aci
12	281	100.0	281	3	AAW28691	Aaw28691 Human AGP
13	281	100.0	281	4	AAW50977	Aaw50977 Human PRO
14	281	100.0	281	4	AAW67243	Aaw67243 Human Apo
15	281	100.0	281	4	AAW11031	Aaw11031 Human TNF
16	281	100.0	281	4	AAW48350	Aaw48350 Human TL2
17	281	100.0	281	5	AAW08133	Aaw08133 Human TRA
18	281	100.0	281	5	AAW31630	Aaw31630 Human TRA
19	281	100.0	281	5	AAW51077	Aaw51077 Human TNF
20	281	100.0	281	5	AAW51077	Aaw51077 Human Apo
21	281	100.0	281	5	AAW51954	Aaw51954 Human Apo
22	281	100.0	281	5	AAW19095	Aaw19095 C neoforn
23	281	100.0	281	5	AAW79593	Aaw79593 Human TNF
24	281	100.0	281	6	ABG73861	Abg73861 Human Apo
25	281	100.0	281	6	ABU10205	Abu10205 Human Apo

26	281	100.0	281	6	ABU71443	Abu71443 Human neo
27	281	100.0	281	6	ABG72738	Abg72738 Human TNF
28	281	100.0	281	6	AAO29543	Aao29543 Human TRA
29	281	100.0	281	6	ABU08558	Abu08558 Human TNF
30	281	100.0	281	6	ABR42313	AbR42313 Human TRA
31	281	100.0	281	6	ABG71905	Abg71905 Human TRA
32	281	100.0	281	6	ABP60546	Abp60546 Human tum
33	281	100.0	281	6	AAE36258	Aae36258 Human TRA
34	281	100.0	281	6	AAO31151	Aao31151 Human TNF
35	281	100.0	281	6	ABO25125	AbO25125 Human TNF
36	281	100.0	281	7	ADB61471	AdB61471 Native hu
37	281	100.0	281	7	ADC35202	AdC35202 Human TNF
38	281	100.0	281	7	ADD14080	AdD14080 Human etc
39	281	100.0	281	7	ADD19010	AdD19010 Human dis
40	281	100.0	281	7	ABW02276	AbW02276 Human TRA
41	281	100.0	281	8	ADE76953	AdE76953 Human pro
42	281	100.0	281	8	ADK72311	AdK72311 Human Apo
43	281	100.0	281	8	ADK72303	AdK72303 Human Apo
44	281	100.0	281	8	ADK72304	AdK72304 Human Apo
45	281	100.0	281	8	ADK72296	AdK72296 Human wil
46	281	100.0	281	8	ADK72310	AdK72310 Human Apo
47	281	100.0	281	8	ADJ63976	AdJ63976 Human apo
48	281	100.0	281	8	ADL71816	AdL71816 Human apo
49	281	100.0	281	8	ADK15498	AdK15498 Human TRA
50	281	100.0	281	8	ADN07587	AdN07587 Human apo
51	281	100.0	281	8	ADR14209	AdR14209 Human NF-
52	281	100.0	281	8	ADK82215	AdK82215 Human TRA
53	281	100.0	281	8	ADS88000	AdS88000 Tumour tr
54	281	100.0	281	8	ABO84415	AbO84415 Human can
55	281	100.0	281	8	ADP23388	AdP23388 PRO poly
56	280	99.6	280	7	ADN95444	AdN95444 Human BEC
57	279	99.3	279	2	AAW76332	Aaw76332 Human TL2
58	279	99.3	279	2	AAW95032	Aaw95032 Tumour ne
59	268	95.4	281	2	AAW27018	Aaw27018 Human Apo
60	263	93.6	281	7	ADB61495	AdB61495 Human Apo
61	262	93.2	281	7	ADB61494	AdB61494 Human Apo
62	254	90.4	281	7	ADB61493	AdB61493 Human Apo
63	248	88.3	281	7	ADB61492	AdB61492 Human Apo
64	244	86.8	281	2	AAW01516	Aaw01516 Protein a
65	242	86.1	266	4	AAW72935	Aaw72935 OmpA sign
66	233	82.9	281	7	ADB61491	AdB61491 Human Apo
67	217	77.2	281	2	AAW27017	Aaw27017 Human Apo
68	202	71.9	281	2	AAW27019	Aaw27019 Human Apo
69	202	71.9	281	2	AAW27016	Aaw27016 Human Apo
70	199	70.8	281	5	ABG72257	Abg72257 Human tum
71	193	68.7	212	5	AAU99301	Aau99301 Human TRA
72	188	66.9	281	8	ADK72306	AdK72306 Human Apo
73	188	66.9	281	8	ADK72313	AdK72313 Human Apo
74	188	66.9	281	8	ADK72305	AdK72305 Human Apo
75	188	66.9	281	8	ADK72309	AdK72309 Human Apo
76	188	66.9	281	8	ADK72308	AdK72308 Human Apo
77	188	66.9	281	8	ADK72312	AdK72312 Human Apo
78	188	66.9	281	8	ADK72307	AdK72307 Human Apo
79	187	66.5	253	4	AAE11037	Aae11037 GH-derive
80	187	66.5	253	6	ABU08564	Abu08564 Human Gro
81	187	66.5	253	8	ADK15507	AdK15507 Human TRA
82	187	66.5	256	4	AAE11038	Aae11038 CMV-deriv
83	187	66.5	256	6	ABU08565	Abu08565 CMV sig.
84	187	66.5	256	8	ADK15509	AdK15509 Human cDN
85	187	66.5	391	8	ADP20791	AdP20791 Fusion co
86	187	66.5	450	7	ADP75172	AdP75172 Fusion co
87	187	66.5	461	5	AAO17496	Aao17496 Antibody-
88	187	66.5	480	5	AAO17495	Aao17495 Antibody-
89	187	66.5	614	5	AAO17494	Aao17494 Antibody-
90	186	66.2	441	3	AAW28692	Aaw28692 FC-huAGP-
91	185	65.8	281	7	ADB61476	AdB61476 Human Apo
92	180	64.1	281	7	ADB61480	AdB61480 Human Apo
93	180	64.1	281	7	ADB61482	AdB61482 Human Apo
94	180	64.1	281	7	ADB61484	AdB61484 Human Apo
95	180	64.1	281	7	ADB61478	AdB61478 Human Apo
96	180	64.1	281	7	ADB61481	AdB61481 Human Apo
97	180	64.1	281	7	ADB61487	AdB61487 Human Apo
98	180	64.1	281	7	ADB61485	AdB61485 Human Apo

99 180 64.1 281 7 ADB61490 Human Apo
100 180 64.1 281 7 ADB61477 Human Apo

ALIGNMENTS

RESULT 1
AAW19777 standard; protein; 281 AA.

XX
AC AAW19777;
DT 22-SEP-1997 (first entry)
DE Novel cytokine Apo-2 ligand.
XX
KW Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.
XX
OS Homo sapiens.
FH Key
FT Peptide
FT Region
FT Protein
FT Region
FT Protein
FT Region
FT Modified-site
FT
FT
FT Protein
FT
FT
XX WO9725428-A1.
PN
XX
PD 17-JUL-1997.
XX
PF 08-JAN-1997; 97WO-US000272.
XX
PR 09-JAN-1996; 96US-00584031.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX
XX WPI; 1997-372867/34.
DR N-PSDB; AAT72796.
XX
PT Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
PT apoptosis for the treatment of breast and colon cancer.
XX
PS Claim 4; Fig 1a; 72pp; English.
XX
CC A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian
CC cell apoptosis. It is believed to be a member of the tumour necrosis
CC factor cytokine family. Its amino acid sequence was deduced from a cDNA
CC clone (AA72796) isolated from a human placental cDNA library. Apo-2
CC ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
CC 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
CC transformed or transfected with a vector contg. Apo-2 ligand nucleic
CC acid. They can be used to induce apoptosis in mammals and to treat
CC pathological conditions such as cancer (esp. breast or colon cancer) or
CC to raise antibodies useful in diagnostic assays
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDDPILLMKSAARNCSWKSQAEYGLY 240
DB 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDDPILLMKSAARNCSWKSQAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 2
AAW27134 standard; protein; 281 AA.
XX
AC AAW27134;
XX
DT 02-APR-1998 (first entry)
XX
DE Human Apoptosis inducing molecule-I (AIM-I).
XX
KW Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
KW tumour necrosis factor ligand superfamily; AIM-I altered expression;
KW neoplasia inhibition; anti-inflammatory agent.
XX
OS Homo sapiens.
XX
FN WO9733899-A1.
XX
PD 18-SEP-1997.
XX
PF 14-MAR-1996; 96WO-US003773.
XX
PR 14-MAR-1996; 96WO-US003773.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM;
XX
XX WPI; 1997-470807/43.
DR N-PSDB; AAT85210.
XX
PT New isolated apoptosis inducing molecule-I - used to develop products for
PT the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
PT versus host disease or inflammation.
XX
PS Claim 2; Fig 1; 82pp; English.
XX
CC The present sequence represents a human Apoptosis inducing molecule-I
CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand
CC superfamily. The products can be used in the diagnosis and treatment of
CC disorders related to under-expression, over-expression or altered
CC expression of AIM-I. AIM-I or agonists can be used for treating
CC autoimmune disorders including systemic lupus erythematosus,
CC immunoproliferative disease lymphadenopathy (IPL),
CC angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit
CC neoplasia such as tumour cell growth, to treat restenosis, to regulate
CC haematopoiesis in endothelial cell development, to stimulate peripheral

CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
 CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or
 CC osteoporosis, for preventing graft-host rejection, and as anti-
 CC inflammatory agents, for treating endotoxic shock or to prevent
 CC activation of HIV
 XX
 XX Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPO 120
 DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPO 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRQEI KENTKNDKQVYIYKTSYPPDILLMKARNCSWKDAEYGLY 240
 DB 181 FYIYSQTYFRQEI KENTKNDKQVYIYKTSYPPDILLMKARNCSWKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 3
 AAW19787
 ID AAW19787 standard; protein; 281 AA.
 XX
 AC AAW19787;
 DT 24-SEP-1997 (first entry)
 XX
 DE Human apoptosis inducer cytokine TRAIL.
 XX
 KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
 KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
 KW thrombotic microangioplasty; therapy.
 XX
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Domain 1..18
 FT Domain /label= Cytoplasmic_domain
 FT Domain 19..38
 FT Domain /label= Transmembrane_domain
 FT Domain 39..281
 FT /label= Extracellular_domain
 FT /note= "contains a receptor-binding region"
 FT Cleavage-site 89..90
 FT /note= "potential KEX2 protease processing site"
 FT Modified-site 109..111
 FT /note= "potential N-glycosylation site"
 FT Cleavage-site 149..150
 FT /note= "potential KEX2 protease processing site"
 XX
 PN WO9701633-A1.
 XX
 PD 16-JAN-1997.
 XX
 PD 25-JUN-1996; 96WO-US010895.
 XX
 PR 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548360.
 XX

PA (IMMV) IMMUNEX CORP.
 XX
 PI Wiley SR, Goodwin RG;
 XX
 DR WPI; 1997-118715/11.
 DR N-PSDB; AAT72847.
 XX
 PT TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
 PT cells - useful for treating thrombotic microangiopathy, cancer and viral
 PT infection and for use in assays.
 XX
 PS Claim 10; Page 43-44; 62pp; English.
 CC
 CC Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
 CC (AAW19787) is a novel cytokine that induces apoptosis of certain target
 CC cells, including cancer cells and virally infected cells. Its amino acid
 CC sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in
 CC vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
 CC polypeptides) can be expressed in host cells and used in the treatment of
 CC cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
 CC to raise antibodies that may be useful for treating thrombotic
 CC microangiopathies
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPO 120
 DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPO 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRQEI KENTKNDKQVYIYKTSYPPDILLMKARNCSWKDAEYGLY 240
 DB 181 FYIYSQTYFRQEI KENTKNDKQVYIYKTSYPPDILLMKARNCSWKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 4
 AAW76829
 ID AAW76829 standard; protein; 281 AA.
 XX
 AC AAW76829;
 DT 25-JAN-1999 (first entry)
 XX
 DE Human TL2 protein.
 XX
 KW TR6; tumour necrosis factor related receptor; human; treatment; stroke;
 KW inflammation; arthritis; septicaemia; autoimmune disease; restenosis;
 KW transplant rejection; infection; ischaemia; brain injury; bone disease;
 KW acute respiratory disease syndrome; acquired autoimmune disease syndrome;
 KW AIDS; cancer; atherosclerosis; Alzheimer's disease; TRAIL; TNF;
 KW TL2; tumour necrosis factor-related apoptosis-inducing ligand.
 XX
 OS Homo sapiens.
 XX
 PN EP870827-A2.
 XX
 PD 14-OCT-1998.
 XX

PF 23-DEC-1997; 97EP-00310562.
 XX 14-MAR-1997; 97US-0041230P.
 PR 09-MAY-1997; 97US-00853684.
 PR 22-AUG-1997; 97US-00916625.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA Deen KC, Young PR;
 XX WPI; 1998-523156/45.
 DR N-PSDB; AAV63096.
 XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding
 PT polypeptide, antibody, agonist, antagonist, etc.
 XX Disclosure; Page 32-33; 34pp; English.
 PS This sequence represents the human tumour necrosis factor (TNF)-related
 XX receptor, TL2 (also known as tumour necrosis factor-related apoptosis-
 CC inducing ligand, TRAIL). This protein is used in a method resulting in
 CC the isolation of the novel human TNF related receptor, TR6. TR6
 CC polypeptides and polynucleotides can be used in the treatment of chronic
 CC and acute inflammation, arthritis, septicemia, autoimmune diseases (e.g.
 CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
 CC host disease, infection, stroke, ischaemia, acute respiratory disease
 CC syndrome, restenosis, brain injury, (acquired autoimmune disease
 CC syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative
 CC disorders), atherosclerosis and Alzheimers disease
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGTCLVLIIVFTVLLQSLCAVAVTVYFTNKLQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGTCLVLIIVFTVLLQSLCAVAVTVYFTNKLQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120
 DB 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQMVYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 RESULT 5
 AAW56760
 ID AAW56760 standard; protein; 281 AA.
 AC AAW56760;
 XX 05-AUG-1998 (first entry)
 DT Human TRAIL polypeptide.
 XX Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
 KW cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 ,FH

FT Domain 1. .18
 FT Region /note= "N-terminal cytoplasmic domain"
 FT 19. .38
 FT Domain /note= "transmembrane region"
 FT 39. .281
 FT Domain /note= "extracellular domain"
 PN US5763223-A.
 XX 09-JUN-1998.
 PD 25-JUN-1996; 96US-00670354.
 XX 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548368.
 XX (IMMV) IMMUNEX CORP.
 PA Goodwin RG, Wiley SR;
 XX WPI; 1998-347322/30.
 DR N-PSDB; AAV29518.
 DR DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful
 PT for producing recombinant polypeptides for research and therapy of
 FT leukaemia, lymphoma, melanoma and viral infections.
 XX Claim 1; Col 33-36; 28pp; English.
 PS This represents a human tumour necrosis factor related apoptosis ligand
 CC (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce
 CC apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful
 CC for producing the recombinant TRAIL polypeptides, which may be useful in
 CC studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
 CC (e.g. to isolate antigens for vaccine development). The polypeptides can
 CC be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
 CC treatment of blood or bone-marrow), or to treat viral infections
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGTCLVLIIVFTVLLQSLCAVAVTVYFTNKLQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGTCLVLIIVFTVLLQSLCAVAVTVYFTNKLQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120
 DB 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQMVYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 RESULT 6
 AAW44354
 ID AAW44354 standard; protein; 281 AA.
 XX AAW44354;
 AC AAW44354;
 XX 28-MAY-1998 (first entry)
 DT
 XX

DE Human AGP-1.
XX Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
KW bone resorption; haematopoietic disease.
XX Homo sapiens.
XX WO9746886-A2.
XX 11-DEC-1997.
XX 06-JUN-1997; 97WO-US009895.
XX 07-JUN-1996; 96US-0060562.
XX (AMGE-) AMGEN INC.
XX Johnson MJ, Simonet WS, Danilenko DM;
PI WPI; 1998-042194/04.
DR N-PSDB; AAV15295.
XX Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -
PT useful for treating inflammation, bone resorption and haematopoietic
PT diseases.
XX Claim 7; Page 36-37; 54pp; English.
XX The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
CC factor (TNF)-related protein, involved in inflammation, myelopoiesis and
CC bone resorption. It has the same nucleic acid and amino acid (aa)
CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or
CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,
CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat
CC haematopoietic diseases associated with reduction in the number of bone
CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
CC by disease, injury or exposure to myelosuppressive agents. Host cells,
CC transformed with expression vectors containing AGP-1 DNA, are used to
CC produce recombinant AGP-1
XX
XX Sequence 281 AA;
Query Match 100.0%; Score 281; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQEIEKENTKNDKQWQYIYKYTSYPPDPILLMKARSCKDAEYGLY 240
DB 181 FYIYSQTYFRQEIEKENTKNDKQWQYIYKYTSYPPDPILLMKARSCKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 7

AAAY01517
ID AAY01517 standard; peptide; 281 AA.
XX AC AAY01517;
XX DT 27-MAY-1999 (first entry)
XX DE Protein associated with neurodegenerative and autoimmune diseases.
XX KW Neurodegenerative disease; autoimmune disease; inflammatory disease;
KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
XX KW surface receptor; TRAIL protein.
XX OS Homo sapiens.
XX PN FR2766713-A1.
XX PD 05-FEB-1999.
XX PF 04-AUG-1997; 97FR-00010176.
XX PR 04-AUG-1997; 97FR-00010176.
XX PA (INNR) BIO MERIEUX.
XX PI Rieger F, Belliveau JF, Perron H;
XX WPI; 1999-156177/14.
XX Use of polypeptide derived from TRAIL protein for diagnosis of
PT degenerative disease - autoimmunity and inflammation, also useful in
PT prevention or treatment, and similar use of corresponding ligand and
PT nucleic acid.
XX PS Claim 2; Page 13; 21pp; French.
XX The specification describes the use a polypeptide corresponding to at
CC least the primary sequence of part of the present sequence to produce a
CC diagnostic, prophylactic or therapeutic composition useful in cases of
CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
CC be used in treatment of neurodegenerative diseases, lupus erythematosus,
CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
CC nervous system cells, antigenic and specifically recognise the surface
CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
CC receptors, inhibiting formation of natural complex
XX SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQEIEKENTKNDKQWQYIYKYTSYPPDPILLMKARSCKDAEYGLY 240
DB 181 FYIYSQTYFRQEIEKENTKNDKQWQYIYKYTSYPPDPILLMKARSCKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8
ID AAY27012 standard; protein; 281 AA.
XX AC AAY27012;
XX DT 24-SEP-1999 (first entry)
XX DE Human Apo-2 ligand (Apo-2L) polypeptide.
XX KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
XX KW lupus; immune-mediated glomerular nephritis; human.
XX OS Homo sapiens.
XX PN WO9936535-A1.
XX PD 22-JUL-1999.
XX PF 15-JAN-1999; 99WO-US001039.
XX PR 15-JAN-1998; 98US-00007886.
XX PR 15-APR-1998; 98US-00060533.
XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;
XX WPI; 1999-444397/37.
XX DR N-PSDB; AAX86987.
XX PT A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
XX PT in mammalian cancer cells.
XX PS Claim 1; Fig 1A; 86pp; English.
XX CC This sequence represents a novel human cytokine, designated Apo-2 ligand
XX CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
XX CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
XX CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
XX CC induce apoptosis for pathological conditions characterized by decreased
XX CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
XX CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
XX CC coding sequence can also be used in quantitative and screening diagnostic
XX CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
XX CC associated with increased apoptosis
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266; Mismatches 0; Indels 0; Gaps 0;
Matches 281; Conservative 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DSDYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSAARNCSWCKDAEYGLY 240
DB 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSAARNCSWCKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFGAFLVG 281
RESULT 9
ID AAY81956 standard; protein; 281 AA.
XX AC AAY81956;
XX DT 10-JUL-2000 (first entry)
XX DE Human Apo-2 ligand protein sequence.
XX KW Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
XX KW therapy; apoptosis; cancer.
XX OS Homo sapiens.
XX PN US6046048-A.
XX PD 04-APR-2000.
XX PF 08-JAN-1997; 97US-00780496.
XX PR 09-JAN-1996; 96US-0009755P.
XX PA (GETH) GENENTECH INC.
XX PI Kim KJ, Ashkenazi AJ, Chuntharapai A;
XX WPI; 2000-282690/24.
XX DR N-PSDB; AAA07425.
XX PT New isolated monoclonal antibodies having antigen specificity for Apo-2
XX PT ligand, e.g. 2G6, 2B11 or 5C2, useful for detecting the expression of Apo
XX PT -2 ligand serum, and for treating diseases associated with increased
XX PT apoptosis.
XX PS Claim 9; Fig 1a; 46pp; English.
XX CC This sequence is the human Apo-2 ligand protein, which is recognised by
XX CC monoclonal antibodies produced by the hybridoma cell lines of the
XX CC invention. The hybridoma cell lines are deposited under the American Type
XX CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
XX CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
XX CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
XX CC tissues, or serum. The antibodies may also be employed as therapeutics.
XX CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
XX CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
XX CC pathological conditions or diseases associated with increased apoptosis.
XX CC They are also useful for the affinity purification of Apo-2 ligand from
XX CC recombinant cell culture or natural sources. The Apo-2 ligand itself may
XX CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266; Mismatches 0; Indels 0; Gaps 0;
Matches 281; Conservative 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DSDYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSAARNCSWCKDAEYGLY 240

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYWDPNDEESMNSPCQVQKWLRLVRLKMLRTSEETISTVQEKQNIPLVRERGPQ 120
DB 61 DSDYWDPNDEESMNSPCQVQKWLRLVRLKMLRTSEETISTVQEKQNIPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSDAEYGLY 240
DB 181 FYIYSQTYFRQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 12

AAB28691
ID AAB28691 standard; protein; 281 AA.

AC AAB28691;

DT 14-FEB-2001 (first entry)

XX Human AGP-1.

KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
KW transplant rejection; cardiovascular disease; arteriosclerosis.

OS Homo sapiens.

XX WO2000063253-A1.

PN 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008004.

XX 16-APR-1999; 99US-00293245.

XX (AMGE-) AMGEN INC.

PI Hsu H, Meng S;

DR WPI; 2000-665240/64.

DR N-PSDB; AAC67831.

PT Fusion protein of AGP-1 protein and an Fc region, used to treat
PT proliferative disorders, immune disorders, and virally-induced disorders.

PS Claim 3; Fig 2; 93pp; English.

XX The present sequence is human AGP-1, a type II transmembrane protein.
CC Fusion proteins comprising an Fc immunoglobulin region fused to the N-
CC terminal portion of the AGP-1 protein have been produced. The fusion
CC proteins can be used to induce apoptosis in a tissue, and to treat
CC proliferative disorders, immune disorders, or virally-induced disorders.
CC The proliferative disorders include cancers, such as breast, prostate,
CC lung or colon cancer. The viral infections include hepatitis, and
CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion
CC proteins have increased biological activity compared to the soluble AGP-1
CC proteins used in prior art therapies

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred No. 2.9e-266; Indels 0; Gaps 0;
Matches 281; Conservative 0; Mismatches 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60

QY 61 DSDYWDPNDEESMNSPCQVQKWLRLVRLKMLRTSEETISTVQEKQNIPLVRERGPQ 120

DB 61 DSDYWDPNDEESMNSPCQVQKWLRLVRLKMLRTSEETISTVQEKQNIPLVRERGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSDAEYGLY 240

DB 181 FYIYSQTYFRQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 13

AAB50977
ID AAB50977 standard; protein; 281 AA.

AC AAB50977;

DT 21-MAR-2001 (first entry)

XX Human PRO1096 protein.

Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
PRO agonist; cancer; inflammatory disorder; immunological disorder.

OS Homo sapiens.

XX WO200073348-A2.

XX 07-DEC-2000.

XX 30-MAY-2000; 2000WO-US014941.

XX 02-JUN-1999; 99WO-US012252.

XX 22-JUN-1999; 99US-0140650P.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 29-OCT-1999; 99US-0162506P.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 09-DEC-1999; 99US-0170282P.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030999.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 02-MAR-2000; 2000WO-US005841.

XX 10-MAR-2000; 2000US-0187202P.

XX 15-MAR-2000; 2000WO-US006319.

XX 30-MAR-2000; 2000WO-US006884.

XX 17-MAY-2000; 2000WO-US008439.

XX 17-MAY-2000; 2000WO-US013705.

PA (GETH) GENENTECH INC.
 XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;
 XX WPI; 2001-016509/02.
 DR N-P5DB; AAC91579.
 XX Twenty eight nucleic acids encoding PRO polypeptides which are useful for
 PT treating various tumors, e.g. breast cancer, and other inflammatory,
 PT angiogenic and immunological disorders.
 XX
 PS Claim 31; Fig 54; 188pp; English.
 XX
 CC The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumors, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukaemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
 CC blastocoeic disorders, and inflammatory, angiogenic and immunological
 CC disorders
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
 Db 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCQVKQWLRLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
 Db 61 DDSYWDPNDEESMNSPCQVKQWLRLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
 Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFQBEIKENTKNDKQVYIYKTSYDPDILLMKSGNSKDAEYGLY 240
 Db 181 FYIYSQTYFRFQBEIKENTKNDKQVYIYKTSYDPDILLMKSGNSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 14
 AAB67243
 ID AAB67243 standard; protein; 281 AA.
 AC AAB67243;
 DT 18-APR-2001 (first entry)
 DE Human Apo2 ligand.
 KW Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
 XX Homo sapiens.
 XX WO200100832-A1.
 PN 04-JAN-2001.
 PD 26-JUN-2000; 2000WO-US017579.
 PF 28-JUN-1999; 99US-0141342P.
 PR

XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
 PI O'connell M, Pai R, Shahrokh Z, Simmons L;
 XX WPI; 2001-123012/13.
 XX Use of divalent metal ions for making Apo-2 ligand and in formulations
 PT containing Apo-2 ligand for increasing yield and stability of ligand
 PT trimers, useful for therapeutic applications.
 XX
 PS Claim 6; Fig 1; 60pp; English.
 XX
 CC The present invention relates to a formulation comprising Apo-2 ligand
 CC and divalent metal ions. Apo-2 ligand and the formulation are useful for
 CC treating cancers and viral infections. Addition of divalent metal ions
 CC for making Apo-2 ligand and formulations containing Apo-2 ligand results
 CC in increased yield and stability of Apo-2 ligand trimers
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
 Db 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCQVKQWLRLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
 Db 61 DDSYWDPNDEESMNSPCQVKQWLRLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
 Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFQBEIKENTKNDKQVYIYKTSYDPDILLMKSGNSKDAEYGLY 240
 Db 181 FYIYSQTYFRFQBEIKENTKNDKQVYIYKTSYDPDILLMKSGNSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 15
 AAE11031
 ID AAE11031 standard; protein; 281 AA.
 XX AAE11031;
 DT 18-DEC-2001 (first entry)
 DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
 KW Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
 KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
 KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
 KW melanoma.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Key 1..18
 FT Domain /label= N_terminal_cytoplasmic_domain
 FT Region 19..38
 FT /label= Transmembrane_region
 FT Domain 39..281
 FT /label= Extracellular_domain
 XX US284236-B1.
 PN

```
XX PD 04-SEP-2001.
XX PF
XX PF 26-MAY-1999; 99US-00320424.
XX PR
XX PR 29-JUN-1995; 95US-00496632.
XX PR 01-NOV-1995; 95US-00548368.
XX PR 25-JUN-1996; 96US-00670354.
XX PR 10-MAR-1998; 98US-00048641.
XX PR 10-NOV-1998; 98US-00190046.
XX PA
XX PA (IMMV ) IMMUNEX CORP.
XX PF
XX PF Wiley SR, Goodwin RG;
XX PF
XX PF WPI; 2001-595463/67.
XX PR
XX PR N-PSDB; AAD18395.
XX PR
XX PR New tumor necrosis factor related apoptosis inducing ligand polypeptides
XX PT for treating viral infections (e.g. bovine viral diarrhea or human
XX PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
XX PS
XX PS Claim 2; Col 45-48; 4lpp; English.
XX CC
XX CC The invention relates to a cytokine designated as tumour necrosis factor
XX CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
XX CC of certain target cells, including cancer cells and virally infected
XX CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
XX CC treating viral infections (e.g. bovine viral diarrhoea or human
XX CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
XX CC melanoma), as a research reagent useful in studying apoptosis including
XX CC the regulation of programmed cell death. TRAIL DNA sequences may be
XX CC employed in developing a gene therapy approach to treating disorders
XX CC mediated by defective or insufficient amounts of TRAIL, in the production
XX CC of TRAIL polypeptides and as probes or primers in polymerase chain
XX CC reactions (PCR). The present sequence is human TRAIL protein
XX CC
XX SQ
XX SQ Sequence 281 AA;
XX SQ Query Match 100.0%; Score 281; DB 4; Length 281;
XX SQ Best Local Similarity 100.0%; Pred. No. 2.9e-266;
XX SQ Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY
XX QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNQLKQMDKYKSGIACFLKE 60
XX DB
XX DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNQLKQMDKYKSGIACFLKE 60
XX QY
XX QY 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
XX DB
XX DB 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
XX QY
XX QY 121 RVAAHITGTRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
XX DB
XX DB 121 RVAAHITGTRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
XX QY
XX QY 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYPPDPILLMKSRNSCWSKDAEYGLY 240
XX DB
XX DB 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYPPDPILLMKSRNSCWSKDAEYGLY 240
XX QY
XX QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
XX DB
XX DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
XX RESULT 16
XX AAB48350
XX ID AAB48350 standard; protein; 281 AA.
XX AC
XX AC AAB48350;
XX DT
XX DT 20-APR-2001 (first entry)
XX DE
XX DE Human TL2 polypeptide.
```

```
XX KW Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TL2;
XX KW anti-inflammatory; immunosuppressive; cerebroprotective; vasotropic;
XX KW antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;
XX KW neutropic; neuroprotective; antiarthritic; antirheumatic; antischemic;
XX KW gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200077191-A1.
XX PD
XX PD 21-DEC-2000.
XX PF
XX PF 12-JUN-2000; 2000WO-US016134.
XX PR
XX PR 15-JUN-1999; 99US-00333593.
XX PA
XX PA (SMIK ) SMITHLINE BEECHAM CORP.
XX PI
XX PI Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;
XX DR
XX DR WPI; 2001-112223/12.
XX DR
XX DR N-PSDB; AAC84745.
XX PT
XX PT New tumor necrosis factor related receptor TR6 polynucleotides and
XX PT polypeptides useful for e.g. for treating chronic and acute inflammation,
XX PT arthritis, septicemia, autoimmune diseases, infection, cancer, bone
XX PT diseases.
XX PS
XX PS Disclosure; Page 26; 47pp; English.
XX CC
XX CC The invention relates to a human tumour necrosis factor (TNF) related
XX CC receptor, TR6. TR6 can be expressed by standard recombinant methodology.
XX CC The TR6 polypeptides are useful for treating chronic and acute
XX CC inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g.
XX CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
XX CC host disease, infection, stroke, ischaemia, acute respiratory disease
XX CC syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,
XX CC atherosclerosis, and Alzheimer's disease. These may also be used to
XX CC inhibit production of TNF-alpha and eicosanoids, as research reagents and
XX CC materials for discovering treatments and diagnostics to animal and human
XX CC diseases. The polypeptides may further be used as immunogens to produce
XX CC antibodies immunospecific for the TR6 polypeptides. The polynucleotides
XX CC may also be used as hybridization probes for cDNA and genomic DNA, for
XX CC isolating full-length cDNAs and genomic clones encoding TR6 and of other
XX CC genes having high sequence similarity to TR6 gene, and for chromosome
XX CC identification. The present sequence represents a human TL2 polypeptide.
XX CC TL2 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and is
XX CC a ligand for the TL2 polypeptide
XX SQ
XX SQ Sequence 281 AA;
XX SQ Query Match 100.0%; Score 281; DB 4; Length 281;
XX SQ Best Local Similarity 100.0%; Pred. No. 2.9e-266;
XX SQ Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY
XX QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNQLKQMDKYKSGIACFLKE 60
XX DB
XX DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNQLKQMDKYKSGIACFLKE 60
XX QY
XX QY 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
XX DB
XX DB 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
XX QY
XX QY 121 RVAAHITGTRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
XX DB
XX DB 121 RVAAHITGTRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
XX QY
XX QY 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYPPDPILLMKSRNSCWSKDAEYGLY 240
XX DB
XX DB 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYPPDPILLMKSRNSCWSKDAEYGLY 240
XX QY
XX QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
```

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Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
|||||
RESULT 17
ABB08133
ID ABB08133 standard; protein; 281 AA.
XX
XX
AC ABB08133;
XX
XX 10-SEP-2002 (first entry)
DT
XX
DE Human TRAIL polypeptide.
XX
KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;
KW tuberculostatic; cytostatic; human; TRAIL.
XX
XX Homo sapiens.
XX
XX WO200236141-A2.
PN
XX
XX 10-MAY-2002.
PD
XX
XX 30-OCT-2001; 2001WO-US044834.
PF
XX
XX 02-NOV-2000; 2000US-0245721P.
PR
XX
XX (IMMV ) IMMUNEX CORP.
PA
XX
XX Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;
PI Thomas EK;
PI
XX
XX WPI; 2002-500114/53.
DR
XX
XX Treating an individual suffering from infection, e.g. inflammation,
PT chickenpox or AIDS, by administering a combination of dendritic cell
PT mobilization factor or maturation agent, T cell enhancing factor and
PT antigen-specific T cells.
XX
XX Disclosure; Page 40-42; 43pp; English.
PS
XX
XX The invention relates to treating an individual at risk for or suffering
CC from infection with a pathogenic or opportunistic organism. The method
CC involves administering a combination of two to five agents comprising:
CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
CC or (e) activated, antigen-specific T cells. The methods are useful for
CC treating an individual at risk for or suffering from infection with a
CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
CC T. cruzi, which causes Chaga's disease). The methods are especially
CC useful for treating an individual suffering from immunosuppression by
CC enhancing a lymphocyte-mediated immune response. In particular, the
CC method is useful for treating inflammations, chickenpox, oral or genital
CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T
CC cell leukemia or T cell lymphoma. The activated antigen-presenting
CC dendritic cells are useful as a vaccine adjuvant. The present sequence
CC represents a human TRAIL polypeptide fragment
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60
|||||
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60
|||||
QY 61 DSYNDPNDDEESNNSPCWQVKQLRQLVRKMLIRTSSEETISTVQEKQNNISPLVRERGPO 120
|||||
DB 61 DSYNDPNDDEESNNSPCWQVKQLRQLVRKMLIRTSSEETISTVQEKQNNISPLVRERGPO 120
|||||

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QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHURNGLVTHEKG 180
|||||
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHURNGLVTHEKG 180
|||||
QY 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPDPILLMKARNSCWSKDAEYGLY 240
|||||
DB 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPDPILLMKARNSCWSKDAEYGLY 240
|||||
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
|||||
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
|||||

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RESULT 18
ABG31630
ID ABG31630 standard; protein; 281 AA.
XX
XX ABG31630;
AC
XX
XX 29-NOV-2002 (first entry)
DT
XX
XX Human TRAIL protein.
DE
XX
XX Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;
KW dendritic cell maturation agent; T cell enhancing factor; skin cancer;
KW antigen-specific T cell; prostate cancer; liver cancer; bone tumour;
KW brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;
KW actinic keratosis; dendritic cell maturation stimulator; cytostatic;
KW dendritic cell activator; T cell enhancer; human; TRAIL.
XX
XX Homo sapiens.
OS
XX
XX WO200266044-A2.
PN
XX
XX 29-AUG-2002.
PD
XX
XX 23-OCT-2001; 2001WO-US046254.
PF
XX
XX 24-OCT-2000; 2000US-0242868P.
PR
XX
XX (IMMV ) IMMUNEX CORP.
PA
XX
XX Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;
PI WPI; 2002-674891/72.
PI
XX
XX Treating an individual with tumors or cancers, e.g. liver cancer or brain
PT tumor, by administering a combination of dendritic cell populations, T
PT cell enhancing factors and activated, antigen-specific T cells.
XX
XX Disclosure; Page 41-43; 44pp; English.
PS
XX
XX The present invention relates to a new method for treating a tumour-
CC bearing subject. The method involves administering a combination of 2 to
CC 5 agents comprising dendritic cell mobilisation factor, dendritic cell
CC maturation agent, tumour-killing agent, T cell enhancing factor or
CC activated, antigen-specific T cells. The method is useful for treating
CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver
CC cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or
CC cervical intraepithelial neoplasia. The present amino acid sequence
CC represents the human TRAIL protein that was used in the method of the
CC invention
XX
XX Sequence 281 AA;
SQ

```

```

Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60
|||||
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60
|||||

```

```
QY 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120
DB 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 19
AAU75062
ID AAU75062 standard; protein; 281 AA.
XX
AC AAU75062;
XX
DT 23-APR-2002 (first entry)
XX
DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
XX
KW TRAIL; TNF; apoptosis; tumour; death domain receptor ligand;
KW diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1; carcinoma;
KW mammary adenocarcinoma; non-small cell lung carcinoma;
KW neurological malignancy; haematological malignancy; lichen planus;
KW non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;
KW malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
KW non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
KW T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
KW discoid lupus erythematosus; human.
XX
OS Homo sapiens.
XX
FN US6329148-B1.
XX
PD 11-DEC-2001.
XX
PF 15-FEB-2000; 2000US-00505250.
XX
PR 16-FEB-1999; 99US-0120313P.
PR 20-AUG-1999; 99US-0149989P.
XX
(STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI Rosen GD, Kao P;
XX
DR WPI; 2002-121125/16.
DR N-PSDB; ABK13192.
XX
Use of a synergistic combination of death domain receptor ligands and
diterpenoid triepoxides for killing of tumor cells.
XX
Disclosure; Col 17-20; 20pp; English.
```

This invention relates to a novel method for enhanced killing of tumour cells comprising contacting a tumour cell with a synergistic combination of a death domain receptor ligand and a diterpenoid triepoxide. This method has cytostatic activity and works by blocking TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the invention may be used for treating tumours, particularly solid tumours, e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma also neurological malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered

CC with other active agents, e.g. anti- metastatic, anti-tumour or anti-
CC angiogenic agents. The potent synergy between the diterpenoids and the
CC death domain ligands allows increased killing at equivalent or lower
CC doses, and can sensitize otherwise resistant cells. This sequence
CC represents the human TNF related apoptosis inducing ligand (TRAIL)
CC protein sequence. TRAIL is a death domain receptor used in the used
CC method of the invention in combination with diterpenoid triepoxides to
CC kill tumours by induction of apoptosis
XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVAVTVVYFTNELKOMQDKYSKGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVAVTVVYFTNELKOMQDKYSKGIACFLKE 60
QY 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120
DB 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 281
```

RESULT 20

```
AAU51077
ID AAU51077 standard; protein; 281 AA.
XX
AC AAU51077;
XX
DT 30-MAY-2002 (first entry)
XX
DE Human Apo-2 ligand (TRAIL).
XX
KW Apo-2 ligand; Apo-2L; TRAIL; human; apoptosis; colorectal cancer; tumour;
KW antitumour; therapy.
XX
OS Homo sapiens.
```

```
Key Location/Qualifiers
Protein 114..281
/note= "Apo-2L polypeptide used in method of Claim 18"
WO200209755-A2.
07-FEB-2002.
```

```
27-JUL-2001; 2001WO-US023691.
27-JUL-2000; 2000US-0221256P.
(GETH ) GENENTECH INC.
Escandon E, Fox JA, Kelley SK, Xiang H;
WPI; 2002-268997/31.
Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I
inhibitor class, and Apo-2 ligand receptor agonist for enhancing
apoptosis in mammalian cells, or for treating cancer in a mammal.
```

PS Claim 18; Page 79-80; 84pp; English.

XX The present sequence is that of human Apo-2 ligand (Apo-2L or TRAIL). The

CC invention relates to methods of inducing apoptosis in mammalian cells,

CC and especially to the use of Apo-2L receptor agonists and CPT-11 (a

CC chemotherapeutic agent of the topoisomerase I inhibitor class) to

CC synergistically induce apoptosis in mammalian cells, in particular

CC mammalian cancer cells, and especially colorectal cancer cells (claimed).

CC The cells may be in cell culture or in a mammal, e.g. a mammal suffering

CC from cancer or a condition in which induction of apoptosis in the cells

CC is desirable. A claimed method of treating cancer in a mammal comprises

CC administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is

CC administered about 6-72 hours prior to administration of the Apo-2L

CC receptor agonist. Preferred Apo-2L receptor agonists include Apo-2L

CC (especially amino acids 114-281 of the present sequence) and anti-DR4 or

CC anti-DR5 receptor antibodies. Exposure of the cancer cells to CPT-11 and

CC Apo-2L receptor agonist leads to upregulation of DR4 and DR5 receptors,

CC directing the cells towards an apoptotic pathway rather than cell cycle

CC arrest and possible DNA repair, thus providing enhanced anticancer

CC activity. An example illustrates the synergistic inhibition of tumour

CC growth by Apo-2L and CPT-11 in athymic nude mice injected s.c. with human

CC COLO205 colon carcinoma cells

XX Sequence 281 AA;

PS Query Match 100.0%; Score 281; DB 5; Length 281;

XX Best Local Similarity 100.0%; Pred. No. 2.9e-266;

XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYNDPNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

DB 61 DDSYNDPNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKSGARNSCWSDAEYGLY 240

DB 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKSGARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 21

ABP51954

ID ABP51954 standard; protein; 281 AA.

XX AC ABP51954;

XX DT 09-OCT-2002 (first entry)

XX DE Human Apo-2 ligand protein sequence SEQ ID NO:4.

XX KW Bacterial host; protease; degp; prc; spr; anti-VEGF antibody; antibody;

XX KW humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;

XX KW anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;

XX KW anti-CD11a; Fab'; Fab'2; Fab'2-leucine zipper fusion; anti-VEGF Fab.

XX OS Homo sapiens.

XX PN WO200248376-A2.

XX PD 20-JUN-2002.

XX PF 07-DEC-2001; 2001WO-US047581.

XX

PR 14-DEC-2000; 2000US-0256162P.

PA (GETH) GENENTECH INC.

PI Chen CY;

XX WPI: 2002-583522/62.

XX N-PSDB; ABQ73920.

XX Novel Escherichia coli strain useful for producing polypeptide, deficient

XX in degp and prc encoding protease, and harboring mutant spr gene, product

XX of gene suppresses growth phenotypes of strains harboring prc mutants.

XX Example 1; Fig 4; 63pp; English.

PS The present invention describes an Escherichia coli strain (I) deficient

XX in chromosomal degp and prc encoding protease degp and prc, respectively,

XX and harbouring a mutant spr gene, the product of mutant spr gene

XX suppresses growth phenotypes exhibited by strains harbouring prc mutants.

XX (I) is useful for producing a polypeptide, by culturing (I) comprising

XX nucleic acid encoding the polypeptide, which is heterologous to the

XX strain, such that the nucleic acid is expressed, and recovering the

XX heterologous polypeptide from the strain. The heterologous polypeptide is

XX proteolytically sensitive. Culturing of (I) is performed in a fermentor

XX under conditions of high- or low-cell density fermentation. The

XX polypeptide is recovered from the periplasm or culture medium of the

XX strain. The polypeptide is an antibody (humanised or full-length

XX antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular

XX endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,

XX anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an

XX antibody fragment having a light chain (kappa light chain). The antibody

XX fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18

XX Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper

XX fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-

XX tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti

XX CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18

XX Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence

XX represents a human Apo-2 ligand amino acid sequence from the present

XX invention

XX Sequence 281 AA;

PS Query Match 100.0%; Score 281; DB 5; Length 281;

XX Best Local Similarity 100.0%; Pred. No. 2.9e-266;

XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYNDPNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

DB 61 DDSYNDPNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKSGARNSCWSDAEYGLY 240

DB 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKSGARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 22

AAO19095

ID AAO19095 standard; protein; 281 AA.

XX AC AAO19095;

XX

```
DT 22-NOV-2002 (first entry)
XX C neoformans antigen expressing dendritic cell related protein #4.
XX Human; fungicide; fungal infection; dendritic cell; antigen;
KW Cryptococcus neoformans; vaccine; immunostimulant.
XX Homo sapiens.
XX WO200266053-A2.
XX 29-AUG-2002.
PD 14-DEC-2001; 2001WO-US048288.
XX 04-JAN-2001; 2001US-0259653P.
XX (IMMV ) IMMUNEX CORP.
XX Thomas EK;
XX WPI; 2002-674896/72.
XX Producing a population of activated, Cryptococcus neoformans antigen-
PT presenting dendritic cells for preventing or treating C. neoformans
PT infection comprises causing the obtained dendritic cells to present the
PT antigen.
XX Disclosure; Page 29-30; 32pp; English.
XX The present invention relates to a method of producing a population of
CC activated, Cryptococcus neoformans antigen-presenting dendritic cells,
CC comprising causing the obtained dendritic cells to present the antigen
CC and maturing the dendritic cells. The activated, C. neoformans antigen-
CC expressing dendritic cells are useful for treating, or as vaccines or
CC vaccine adjuvants against, C. neoformans infection, or for generating
CC antigen-specific T cells. The present sequence is a human protein shown
CC in the exemplification of the invention
XX
XX Sequence 281 AA;
Query Match 100.0%; Score 281; DB 5; Length 281;
Beat Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSI-CVAVTVVYFTNELKQMDKYSGGIACFLKE 60
DB 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLCVAVTVVYFTNELKQMDKYSGGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLIRTSSEITISTVQSKQNI SPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLIRTSSEITISTVQSKQNI SPLVRERGQ 120
QY 121 RVAAHITGRSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRQERIKENTKNDKQMVQYIKYTSYPPDILLMKSRNSCKDAEYGLY 240
DB 181 FYIYSQTYFRQERIKENTKNDKQMVQYIKYTSYPPDILLMKSRNSCKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
RESULT 23
AAU79593
ID AAU79593 standard; protein; 281 AA.
XX
XX AAU79593;
AC
XX 24-SEP-2002 (first entry)
```

```
XX DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.
XX KW Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
KW TRAIL; apoptosis; programmed cell death; differentiation; development;
KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
KW chromosome 3q26.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX Domain 1..16
FT /note= "Cytoplasmic domain"
FT Domain 17..38
FT /note= "Transmembrane domain"
FT Domain 39..281
FT /note= "Extracellular domain"
FT Domain 118..256
FT /note= "TNF domain"
XX
XX US2002061525-A1.
XX 23-MAY-2002.
XX 16-MAY-2001; 2001US-00855544.
XX 16-MAY-2000; 2000IL-00136156.
XX (YELI/) YELIN R.
XX (KHOS/) KHOSRAVI R.
XX (SAVI/) SAVITZKY K.
XX Yelin R, Khosravi R, Savitzky K;
XX WPI; 2002-479259/51.
XX New splice variants of tumor necrosis factor-related apoptosis inducing
PT ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat
PT diseases or disorders associated with low expression of the variants.
XX Disclosure; Fig 9; 29pp; English.
XX The invention discloses isolated, naturally occurring, polypeptide splice
CC variants of human tumour necrosis factor (TNF)-related apoptosis inducing
CC ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal
CC cellular differentiation and development of multicellular organisms.
CC Apoptosis is induced by certain cytokines which include TNF and TRAIL
CC (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane
CC protein which induces apoptosis and nuclear factor-B (NF-B) activation in
CC many tissues and cells. Receptors for TRAIL include two death domain
CC containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1
CC and DcR2, lacking the intracellular signalling death domain. TRAIL,
CC induced by type I interferons, induces apoptosis in tumour cells, whereas
CC normal cells are relatively resistant without showing significant toxic
CC side effects. Thus, TRAIL has the potential to be a very useful
CC antitumour agent. The naturally occurring splice variants may differ in
CC their cellular distribution, expression levels/timing and activity.
CC Determining these factors could provide possible mechanisms for the
CC induction of apoptosis of tumours cells. The splice variant polypeptides
CC and polynucleotides can be used in gene therapy, to raise antibodies, to
CC detect the levels, distribution and ratios of expression of TRAIL, and
CC its splice variants, in a biological sample and to identify compounds
CC which bind the variant TRAIL products and modulate its activity (agonists
CC and antagonists). Pharmaceutical compositions, comprising an expression
CC vector or any of the amino acid sequences, are useful for causing a
CC cytotoxic effect in cancer cells and for treatment of diseases which can
CC be ameliorated, cured or prevented by lowering or raising the level of
CC the amino acid sequences. The antibodies may also have a therapeutic
CC utility in blocking or decreasing the activity of the TRAIL variant
CC products. Diseases that may be treated include cancer, neurodegenerative
```

CC diseases, autoimmune diseases, diseases involved in the non-normal
CC development of tissues and aging. TRAIL's gene is located on chromosome
CC 3q26. The sequence presented is the wild-type human TNF-related apoptosis
CC inducing ligand (TRAIL) protein
XX
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMVEQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

QY 61 DSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
Db 61 DSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSVPDPIILMKSGARNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSVPDPIILMKSGARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 24
ABG73861
ID ABG73861 standard; protein; 281 AA.
XX AC ABG73861;
XX
DT 03-APR-2003 (first entry)
XX
DE Human Apo-2 ligand protein.
XX
KW Human; Apo-2; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;
KW nuclear factor-kappa B; NF-kappa B; Apo-2 ligand; AIDS;
KW tumour necrosis factor receptor; acquired immunodeficiency syndrome;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW multiple sclerosis; retinitis pigmentosa; cerebellar degeneration;
KW aplastic anaemia; myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; cancer; lupus; herpes virus infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 15..40
FT Domain /note= "Transmembrane domain"
FT Domain 41..281
FT Domain /note= "Extracellular domain"
FT Modified-site 109
FT FT /note= "N-glycosylated"
FT
FN US6462176-B1.
XX
PD 08-OCT-2002.
XX
PF 11-SEP-1997; 97US-00928069.
XX
PR 23-SEP-1996; 96US-0026943P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
XX WPI; 2003-173840/17.
DR

DR N-PSDB; ABX15469.
XX
PT Novel isolated Apo-3 polypeptide useful for inducing apoptosis in
PT mammalian cells, for generating antibodies, in affinity purification
PT techniques, and in competitive-type receptor binding assays.
XX
XX
PS Example 4; Fig 4; 52pp; English.
XX
CC The invention relates to an Apo-3 polypeptide having an extracellular
CC domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide
CC has been found to stimulate or induce apoptotic activity in mammalian
CC cells. Human Apo-3 exhibits similarities to the tumour necrosis factor
CC receptor (TNFR) family of polypeptides. The invention also relates to a
CC chimeric molecule comprising an extracellular domain sequence comprising
CC residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The
CC Apo-3 polypeptide is useful therapeutically to induce apoptosis in
CC mammalian cells. Decreased levels of apoptosis has been associated with
CC conditions such as cancer, lupus, and herpes virus infection. Increased
CC levels of apoptosis are associated with diseases such as acquired
CC immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis
CC pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial
CC infarction, stroke, reperfusion injury, and toxin-induced liver disease.
CC The Apo-3 polypeptide is also useful in non-therapeutic applications such
CC as in quantitative diagnostic assays as a control against which samples
CC containing unknown quantities of Apo-3 may be prepared, in generating
CC antibodies, as standards in assays for Apo-3, in affinity purification
CC techniques, and in competitive-type receptor binding assays. The chimeric
CC molecule is useful therapeutically to inhibit apoptosis or nuclear factor
CC -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-
CC Apo-3 antibodies. The present sequence represents polypeptide sequence of
CC the human Apo-2 ligand protein which is also reported to be involved in
CC apoptotic cell death. In the current invention the apoptotic activity of
CC the Apo-2 ligand protein was measured on human lymphoid cells
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMVEQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

QY 61 DSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
Db 61 DSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSVPDPIILMKSGARNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSVPDPIILMKSGARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 25
ABU10205
ID ABU10205 standard; protein; 281 AA.
XX AC ABU10205;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human Apo-2 ligand.
XX
KW Human; Apo-2 ligand; apoptosis; gene therapy; inflammation; cancer;
XX

KW neurodegenerative disease; immunosuppressive; tissue typing.
OS Homo sapiens.
XX US2003004313-A1.
XX 02-JAN-2003.
XX 28-MAR-2002; 2002US-00112193.
XX 23-SEP-1996; 96US-0026943P.
PR 11-SEP-1997; 97US-00928069.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ;
XX WPI; 2003-438872/41.
DR N-PSDB; ACA61696.
XX New isolated Apo-3 polypeptides, useful for stimulating or inducing
PT apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo
PT or ex vivo gene therapy techniques.
XX Example 4; Fig 4; 50pp; English.
XX The invention relates to an isolated Apo-3 polypeptide. The Apo-3
CC polypeptides are useful for stimulating or inducing apoptotic activity in
CC mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy
CC techniques. The Apo-3 chimeric molecules are useful for inhibiting
CC apoptosis, or as immunogens used in generating antibodies. The
CC antagonistic antibodies may be used to block excessive apoptosis, for
CC instance in neurodegenerative disease, or to block potential autoimmune/
CC inflammatory effects of Apo-3 resulting from NF-kappaB activation. The
CC nucleic acid sequences are useful as diagnostics for tissue-specific
CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or
CC knockout animals. The transgenic or knockout animals are useful in
CC developing and screening of therapeutically useful reagents. The present
CC sequence represents the amino acid sequence of human Apo-2 ligand
XX Sequence 281 AA;
SQ Query Match 100.0%; Score 281; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNKLQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNKLQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDESMNSPCQWKQLRQKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DDSYWDPNDESMNSPCQWKQLRQKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRQBEIKENTKNDKQVYIYKTSYPPDILLMKSNCSWKAIEYGLY 240
DB 181 FYYIYSQTYFRQBEIKENTKNDKQVYIYKTSYPPDILLMKSNCSWKAIEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFVNG 281
DB 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFVNG 281
RESULT 26
ABU71443
ID ABU71443 standard; protein; 281 AA.
XX
AC ABU71443;
XX

DT 09-JUN-2003 (first entry)
XX Human neoplasia inhibiting PRO polypeptide PRO1096.
DE
XX
KW Human; tumour; cancer; neoplasia; liver cancer; sarcoma; breast cancer;
KW ovarian cancer; renal cancer; colorectal cancer; melanoma;
KW uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
KW gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;
KW central nervous system cancer; hepatic carcinoma; glioblastoma;
KW neuronal disorder; glial disorder; astrocytal disorder;
KW hypothalamic disorder; glandular disorder; macrophagial disorder;
KW epithelial disorder; stromal disorder; blastocoelec disorder;
KW inflammatory disorder; angiogenic disorder; immunologic disorder.
XX Homo sapiens.
OS
XX US2002192209-A1.
XX 19-DEC-2002.
XX 30-NOV-2001; 2001US-00001054.
XX 17-SEP-1997; 97US-0059114P.
PR 27-MAR-1998; 98US-0079689P.
PR 30-MAR-1998; 98US-0079920P.
PR 24-APR-1998; 98US-0082999P.
PR 29-APR-1998; 98US-0083545P.
PR 12-MAY-1998; 98US-0085149P.
PR 02-JUN-1998; 98US-0087607P.
PR 11-JUN-1998; 98US-0088858P.
PR 25-JUN-1998; 98US-0090691P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100263P.
PR 15-SEP-1998; 98US-0100390P.
PR 23-SEP-1998; 98US-0101476P.
PR 18-NOV-1998; 98US-0107783P.
PR 18-NOV-1998; 98US-0108849P.
PR 19-NOV-1998; 98US-00180997.
PR 15-DEC-1998; 98US-0112420P.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 12-JAN-1999; 99US-0115554P.
PR 12-JAN-1999; 99US-0115558P.
PR 20-JAN-1999; 99US-0116533P.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-APR-1999; 99US-00284291.
PR 20-APR-1999; 99WO-US008615.
PR 27-APR-1999; 99US-0131294P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0140650P.
PR 20-JUL-1999; 99US-0144758P.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 09-SEP-1999; 99US-00380913.
PR 18-OCT-1999; 99US-00403297.
PR 29-OCT-1999; 99US-0162506P.
PR 10-NOV-1999; 99US-00423741.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028634.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.

FT FT /note= "N-terminal fragment specifically claimed in claim
 26"
 124. .276
 FT FT /note= "This region is specifically claimed in claim 20"
 276. .281
 FT FT /note= "C-terminal fragment specifically claimed in claim
 26"
 FT FT
 XX US6521228-B1.
 PN
 XX
 PD 18-FEB-2003.
 XX
 XX 02-APR-2001; 2001US-00825563.
 PF
 XX 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548368.
 PR 25-JUN-1996; 96US-00670354.
 PR 26-MAR-1998; 98US-00048641.
 PR 10-NOV-1998; 98US-00190046.
 PR 26-MAY-1999; 99US-00320424.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 XX Wiley SR, Goodwin RG;
 XX
 DR WPI; 2003-340628/32.
 DR N-PSDB; ABX93869.
 XX
 XX Novel antibody which binds to human tumor necrosis factor related
 PT apoptosis inducing ligand protein, useful for inhibiting TRAIL-mediated
 PT apoptosis of a target cell, or blocking binding of TRAIL to a target
 PT cell.
 FT
 PS Claim 1; Col 45-48; 40pp; English.
 XX
 CC The invention relates to an antibody that specifically binds: (a) the
 CC human tumor necrosis factor (TNF) related apoptosis inducing ligand
 CC (TRAIL) protein appearing as AB008558; (b) a soluble human TRAIL
 CC polypeptide; (c) a polypeptide comprising amino acids 124-276 of
 CC AB008558, or (d) a fragment of the TRAIL protein. Also included is an
 CC antigen-binding fragment of the antibody (a monoclonal antibody), a
 CC hybridoma cell line that produces the antibody. The antibody is used in
 CC assays to detect the presence of TRAIL polypeptides, either in vitro or
 CC in vivo, purifying TRAIL by affinity chromatography, blocking binding of
 CC TRAIL to target cells and thus inhibiting a biological activity of TRAIL.
 CC The antibody is useful for treating disorders mediated or exacerbated by
 CC TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic
 CC thrombocytopenic purpura (TTP), adult haemolytic uraemic syndrome (HUS)
 CC (even though it can strike children as well), small blood vessel clotting
 CC disorders e.g., cardiac problems in paediatric AIDS patients and systemic
 CC lupus erythematosus (SLE). The present sequence represents human TRAIL
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVVYFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKMLRILTSEETISTVQEKQKNISPLVRERGQ 120
 DB 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKMLRILTSEETISTVQEKQKNISPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWSSRSGHSFLSNLHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWSSRSGHSFLSNLHLRNGELVIHEKG 180
 QY 181 FYIYISQTYFRQEETIKENTKNDKQWQVIYKYTSPDPDILLMKARNSCWSDAEYGLY 240
 DB 181 FYIYISQTYFRQEETIKENTKNDKQWQVIYKYTSPDPDILLMKARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASPFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASPFGAFLVG 281
 RESULT 30
 ABR42313
 ID ABR42313 standard; protein; 281 AA.
 XX
 AC ABR42313;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Human TRAIL protein.
 XX
 KW Human; TRAIL; tumour necrosis factor; ligand; cytostatic;
 KW immunomodulator; osteopathic.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040307-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 25-JUL-2002; 2002WO-US023782.
 XX
 PR 27-JUL-2001; 2001US-0307838P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Hilbert DH, Rosen CA;
 XX
 DR WPI; 2003-430659/40.
 DR N-PSDB; ACC57899.
 XX
 XX New heteromultimeric complex having a first polypeptide member of the
 PT tumor necrosis factor (TNF) ligand family, and a second different member
 PT of TNF ligand family, useful for treating cancer, osteoporosis or an
 PT autoimmune disease.
 XX
 PS Disclosure; Page 364-365; 388pp; English.
 XX
 CC The present sequence is the protein sequence of human TRAIL polypeptide.
 CC The invention relates to compositions comprising heterotrimeric complexes
 CC of tumour necrosis factor (TNF) ligand family members, and their use in
 CC the detection, prevention and treatment of disease. In one embodiment,
 CC the heterotrimeric complex comprises full-length or extracellular
 CC portions of TRAIL and full-length or extracellular portions of other TNF
 CC ligand family members, preferably RANKL. The heterotrimeric complexes of
 CC the invention are useful for treating an autoimmune disease, cancer or
 CC osteoporosis, and particularly for inhibiting cancer cell proliferation,
 CC increasing B cell proliferation, or inducing apoptosis of T cells. A
 CC claimed method of inducing apoptosis of T cells comprises administering a
 CC heterotrimeric complex consisting of FasL and LIGHT, TNF-alpha,
 CC lymphotoxin-beta or TRAIL. A claimed method of inhibiting cancer cell
 CC proliferation involves administering a heterotrimeric complex consisting
 CC of TRAIL and CD40L or RANK. A claimed method of treating osteoporosis
 CC comprises administering an antibody against a complex comprising RANKL
 CC and TRAIL
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVVYFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVKMLRILTSEETISTVQEKQKNISPLVRERGQ 120

Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 Qy 121 RVAAHITGRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
 Db 121 RVAAHITGRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
 Qy 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSARNCSWSDAEYGLY 240
 Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSARNCSWSDAEYGLY 240
 Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 31

ID ABG71905 standard; protein; 281 AA.

AC ABG71905;

DT 20-JAN-2003 (first entry)

XX Human TRAIL receptor-associated protein.

XX Human; TRAIL receptor; tumour necrosis factor; TNF;

KW light chain variable region TNF-related apoptosis-inducing ligand;

KW antibody; VH; VL; cancer; heavy chain variable region; TR4; TR5; TR7;

KW TR10; apoptosis; hyperproliferative disorder; hybridoma cell line;

KW Kaposi's sarcoma; graft-versus-host disease; GVHD; infectious disease;

KW AIDS; acquired immunodeficiency syndrome; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; autoimmune disorder;

KW multiple sclerosis; Behcet's disease; lupus erythematosus;

KW inflammatory disease; rheumatoid arthritis; psoriasis; wound healing;

KW cardiovascular disorder; angiogenesis; immune response;

KW chemotherapeutic agent.

XX Homo sapiens.

XX WO200279377-A2.

XX 10-OCT-2002.

XX 07-NOV-2001; 2001WO-US042996.

XX 08-NOV-2000; 2000US-0246612P.

XX 16-NOV-2000; 2000US-0248847P.

XX 27-NOV-2000; 2000US-0252904P.

XX 04-JUN-2001; 2001US-0295018P.

XX 09-OCT-2001; 2001US-0327359P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Salcedo T, Roschke V, Ruben SM, Rosen CA;

XX WPI; 2003-040669/03.

XX Novel antibody for treating, or preventing disease or disorder, comprises

XX amino acid sequence having identity to other amino acid sequence of

XX either variable heavy/light chain-complementarity determining regions.

XX Disclosure; Page 366; 375pp; English.

XX The invention relates to an isolated antibody comprising a first amino

XX acid sequence having 95 % identity to a second amino acid sequence of

XX either variable heavy chain or light chain-complementarity determining

XX regions (VHCDR1)/VHCDR2/VHCDR3 or VHCDR3/VHCDR2/VHCDR3 appearing as

XX ABG71906-ABG71911 being specific for human TRAIL receptors 1-4 (TNF

XX (tumour necrosis factor)-related apoptosis-inducing ligand receptor, also

XX known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that

XX produces the antibody, an antibody that binds the same epitope on a TR4

XX polypeptide as the antibodies detailed above, detecting expression of a

XX TR4 polypeptide(or detecting, diagnosing, prognosis or monitoring

CC cancers, and other hyperproliferative disorders) using the antibodies, a
 CC hybridoma cell line selected from the hybridoma cell lines contained in
 CC ATCC Deposit No. PTA-3149, PTA-2687, PTA-3369, PTA-2730, PTA-2729, PTA-
 CC 2728, PTA-3368, and PTA-2731 and the antibodies expressed by these
 CC hybridoma cell lines. The antibodies of the invention are useful for
 CC diagnosing or treating a disease or disorder associated with increased or
 CC decreased apoptosis, e.g. cancer (such as colon, breast, uterine,
 CC pancreatic, lung, gastrointestinal, and Kaposi's sarcoma), graft-versus-
 CC host disease (GVHD), infectious disease, acquired immunodeficiency
 CC syndrome (AIDS), or neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disease), autoimmune disorders like multiple
 CC sclerosis, Behcet's disease, lupus erythematosus, inflammatory diseases
 CC such as rheumatoid arthritis, and psoriasis, cardiovascular disorders, in
 CC promoting angiogenesis, wound healing, and in regulating immune response.
 CC Many other diseases and disorders are listed in the specification. The
 CC antibody is administered in combination with a chemotherapeutic agent
 CC selected from irinotecan, paclitaxel (TAXOL (RPM)), and gemcitabine. The
 CC antibody is useful as a diagnostic tool to monitor the expression of
 CC TRAIL receptor expression on cells, to detect, purify, and target the
 CC polypeptides, and in immunoassays for qualitatively and quantitatively
 CC measuring levels of TRAIL receptor polypeptides. The present sequence is
 CC a human TRAIL receptor associated protein. Note: The present sequence is
 CC included in the sequence listing but is not referred to anywhere else in
 CC the specification

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.9e-266;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNELKQMDKYKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNELKQMDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

Qy 121 RVAAHITGRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

Db 121 RVAAHITGRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

Qy 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSARNCSWSDAEYGLY 240

Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSARNCSWSDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 32

ABP60546

ID ABP60546 standard; protein; 281 AA.

XX AC ABP60546;

XX 28-MAR-2003 (first entry)

XX Human tumour necrosis factor TRAIL.

XX APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;

XX dermatological; immunosuppressive; antiinflammatory; antirheumatic;

XX antiarthritic; cytostatic; antianaemic; antiallergic; antidiabetic;

XX neuroprotective; ophthalmological; tuberculostatic; antidiabetic;

XX antiproliferative; anti-HIV; antiarteriosclerotic; vasotroplic; thyromimetic;

XX haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;

XX inflammatory disorder; proliferative disorder; single chain antibody;

XX antibody; human; TRAIL; tumour necrosis factor.

XX Homo sapiens.

OS XX

PN WO200294192-A2.
 XX 28-NOV-2002.
 PD 22-MAY-2002; 2002WO-US016106.
 PF 24-MAY-2001; 2001US-0293100P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM;
 PI WPI; 2003-156740/15.
 DR Novel isolated antibody that immunospecifically binds tumor necrosis
 XX factor delta, useful for treating, preventing or ameliorating Non-
 PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
 PT syndrome.
 XX Disclosure; Page 216-217; 225pp; English.
 PS The invention relates to a novel antibody or its fragment, which
 CC immunospecifically binds tumor necrosis factor Delta (TNF-delta/APRIL).
 CC The antibody of the invention has dermatological, immunosuppressive,
 CC anti-inflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,
 CC antiallergic, antiasthmatic, neuroprotective, ophthalmological,
 CC tuberculosic, antidiabetic, antipsoriatic, anti-HIV,
 CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
 CC The antibody or its fragment are useful for treating, preventing or
 CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
 CC human, disease or disorder such as autoimmune disease, and graft versus
 CC host disease (GVHD). The autoimmune disease is systemic lupus
 CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or
 CC ameliorating a disease or disorder associated with aberrant APRIL or
 CC APRIL receptor expression or aberrant function of APRIL or APRIL
 CC receptor. The disease or disorders includes autoimmune and inflammatory
 CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
 CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
 CC system, particularly B cell cancers, immune disorders such as myasthenia
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 CC proliferative disorders (e.g. leukemia). The present sequence represents
 CC the tumor necrosis factor TRAIL
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVITVLQSLCVAVTVYFTNKLQMDKYKSGIACFLKE 60
 Db 1 MAMMEVQGGPSLGQTCVLIVITVLQSLCVAVTVYFTNKLQMDKYKSGIACFLKE 60
 QY 61 DSDYNDPNDDESNPCWQVKVQLRQVVKMLRTSEETISTVQEKQNPISPLVRERGQ 120
 Db 61 DSDYNDPNDDESNPCWQVKVQLRQVVKMLRTSEETISTVQEKQNPISPLVRERGQ 120
 QY 121 RVAAMHTGTGRSNTLSSPNKNEKALGRKINSWESSRSGHFLNLHRLNGELVIHEKG 180
 Db 121 RVAAMHTGTGRSNTLSSPNKNEKALGRKINSWESSRSGHFLNLHRLNGELVIHEKG 180
 QY 181 FYIYISQTYFRQEEIKENTKDKQWQVIYKYTSYDPDPILLMKSNCSWKDAEYGLY 240
 Db 181 FYIYISQTYFRQEEIKENTKDKQWQVIYKYTSYDPDPILLMKSNCSWKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFVLG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFVLG 281

RESULT 33
 AAE36258
 ID AAE36258 standard; protein; 281 AA.
 XX AC AAE36258;
 DT 26-JUN-2003 (first entry)
 XX DE Human TR4 ligand, TRAIL protein.
 XX TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;
 KW hyperproliferative disorder; neurodegenerative disorder; immune disorder;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis;
 KW rheumatoid arthritis; multiple sclerosis; Sjogren's disease; asthma;
 KW biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;
 KW glomerulonephritis; immune deficiency syndrome; myasthenia gravis;
 KW polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;
 KW infectious disease; acquired immunodeficiency syndrome; viral infection;
 KW AIDS; proliferative disorder; myocardial infarction; reperfusion injury; cachexia;
 KW ischaemic injury; myocardial infarction; reperfusion injury; cachexia;
 KW anorexia; stroke; cardiovascular disorder; peripheral artery disease;
 KW limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;
 KW ocular disorder; wound healing; angiogenesis; transplantation; human.
 XX Homo sapiens.
 OS WO200297033-A2.
 XX 05-DEC-2002.
 XX 07-MAY-2002; 2002WO-US014268.
 XX 25-MAY-2001; 2001US-0293473P.
 PR 04-JUN-2001; 2001US-0294981P.
 PR 02-AUG-2001; 2001US-0309176P.
 PR 21-SEP-2001; 2001US-0323807P.
 PR 09-OCT-2001; 2001US-0327364P.
 PR 07-NOV-2001; 2001US-0331044P.
 PR 14-NOV-2001; 2001US-033110P.
 PR 20-DEC-2001; 2001US-0341237P.
 PR 05-APR-2002; 2002US-0369860P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;
 PI WPI; 2003-140454/13.
 DR Novel antibody useful for treating cancers and other hyperproliferative
 XX disorders, immunospecifically binds to TRAIL receptor and comprises
 PT variable heavy or light chain complementarity determining regions.
 PS Disclosure; Page 300-301; 301pp; English.
 CC The present invention relates to novel antibodies that immunospecifically
 CC bind to TRAIL receptor (TR4). Sequences of the invention are useful for
 CC treating, preventing or ameliorating cancer (e.g. colon, breast, uterine,
 CC pancreatic, lung, gastrointestinal or central nervous system cancer e.g.
 CC medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in
 CC human. They are useful for detecting expression of TR4 polypeptide and
 CC detecting, diagnosing, prognosing or monitoring cancers and other hyper-
 CC proliferative disorders. Antibodies of the invention are useful for
 CC treating, preventing or ameliorating neurodegenerative disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
 CC retinitis pigmentosa, cerebellar degeneration and Huntington's disease),
 CC immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis,
 CC Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease,
 CC polymyositis, immune-related glomerulonephritis, myasthenia gravis,
 CC Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory
 CC disorders (e.g. asthma, allergic disorders and rheumatoid arthritis),
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)),
 CC herpes viral infections and other viral infections) and proliferative

CC disorders. They are also useful for treating myelodysplastic syndromes
 CC (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke,
 CC myocardial infarction and reperfusion injury), septic shock, cachexia,
 CC anorexia and toxin-induced liver diseases (such as alcohol). They are
 CC also useful for treating cardiovascular disorders including peripheral
 CC artery diseases such as limb ischaemia, arrhythmia, congestive heart
 CC failure and cardiovascular tuberculosis, diseases or disorders associated
 CC with neovascularisation and ocular disorders, for wound healing, for
 CC promoting angiogenesis and as adjuvants to enhance immune responsiveness
 CC to specific antigen e.g. viral antigen. They are also useful in the
 CC preparation or recovery from surgery, trauma, radiation therapy and
 CC transplantation. The present sequence is human TR4 ligand, TRAIL protein
 CC used in the invention
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
 DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 QY 181 FYIYISQTYFRFQBEIKENTKNDKQWQYIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240
 DB 181 FYIYISQTYFRFQBEIKENTKNDKQWQYIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240

RESULT 34
 AAO31151
 ID AAO31151 standard; protein; 281 AA.
 AC AAO31151;
 XX
 XX 06-OCT-2003 (first entry)
 XX Human TNF-related apoptosis-inducing ligand (TRAIL).

XX Human; protein coordinate data; heavy chain variable domain; VH; cancer;
 KW complementarity determining region; CDR; light chain variable domain; VL;
 KW TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
 KW DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
 KW Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
 KW glioblastoma; graft versus host disease; antibody therapy; neurotropic;
 KW AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
 KW immunosuppressive; neuroprotective; antibody therapy; antibody.

XX Homo sapiens.
 XX WO2003054216-A2.
 XX
 XX 03-JUL-2003.
 XX
 XX 19-DEC-2002; 2002WO-US040597.
 XX
 XX 20-DEC-2001; 2001US-0341237P.
 PR 05-APR-2002; 2002US-0369877P.
 PR 04-JUN-2002; 2002US-0384828P.
 PR 18-JUL-2002; 2002US-0396591P.
 PR 15-AUG-2002; 2002US-0403370P.

PR 13-NOV-2002; 2002US-0425737P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;
 DR WPI; 2003-569250/53.
 XX
 XX New antibody or its fragment, useful for treating, preventing or
 PT ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
 PT gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
 PT disease, AIDS.
 XX

PS Disclosure; Page 297-298; 301pp; English.

XX The invention relates to an isolated antibody or its fragments such as
 CC VHCDRI (heavy chain variable domain complementarity determining region),
 CC VHCDR2, VHCDR3, VLCDRI (light chain variable domain complementarity
 CC determining region), VLCDR2 or VLCDR3. The antibody or its fragment
 CC immunospecifically binds TRAIL (tumour necrosis factor; TNF-related
 CC apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
 CC TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The
 CC antibody or its fragment is useful for treating, preventing or
 CC ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
 CC gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
 CC nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
 CC graft versus host disease, AIDS (acquired immune deficiency syndrome) or
 CC a neurodegenerative disorder. The invention is useful in antibody
 CC therapy. The present sequence is human TRAIL

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
 DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 QY 181 FYIYISQTYFRFQBEIKENTKNDKQWQYIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240
 DB 181 FYIYISQTYFRFQBEIKENTKNDKQWQYIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 35

ABO25125

ID ABO25125 standard; protein; 281 AA.

XX ABO25125;

XX 05-SEP-2003 (first entry)

XX Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1.

XX Human; DNA methylation; cancer; colon cancer.

XX Homo sapiens.

XX US2003013099-A1.

XX

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PD 16-JAN-2003.
XX
PF 07-MAR-2002; 2002US-00093766.
XX
XX 07-MAR-2001; 2001US-0277380P.
XX
XX (LASEK/) LASEK A K W.
PA (JONE/) JONES D A.
PA (KARP/) KARP A R.
XX
PI Lasek AKW, Jones DA, Karpf AR;
XX
DR WPI: 2003-503249/47.
DR N-PSDB; ACD42246.
XX
XX New combination comprising cDNAs that are expressed in a disorder or
PT process associated with DNA methylation, useful for diagnosing, staging,
PT treating or monitoring treatment of cancer, e.g. colon cancer.
XX
XX Disclosure; Page 56-57; 66pp; English.
XX
XX The invention relates to a combination comprising cDNAs which are
CC expressed in a disorder or process associated with DNA methylation. The
CC combination and cDNAs are useful for diagnosing, staging, treating or
CC monitoring treatment of cancer, e.g. colon cancer and for detecting
CC changes in expression of genes encoding proteins that are associated with
CC DNA methylation. The protein is useful for screening molecules or
CC compounds to identify at least one ligand that binds to the protein and
CC for producing an antibody. The present sequence represents the amino acid
CC sequence of a protein expressed in a disorder or process associated with
CC DNA methylation
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 281; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKQNISPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKQNISPLVRERGQ 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
QY 181 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDILLMKSGARNCSKDAEYGLY 240
DB 181 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDILLMKSGARNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 36
ADB61471
ID ADB61471 standard; protein; 281 AA.
XX
XX ADB61471;
XX
XX 04-DEC-2003 (first entry)
DT
XX Native human Apo-2 ligand protein.
DE
XX Apo-2 ligand; DR5 Apo2L complex; receptor contact region;
KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;

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KW native; human.
XX
XX Homo sapiens.
XX
XX WO2003029420-A2.
XX
XX 10-APR-2003.
XX
XX 01-OCT-2002; 2002WO-US031210.
XX
XX 02-OCT-2001; 2001US-0326622P.
XX (GETH ) GENENTECH INC.
XX
XX Kelley RF, Lindstrom SH;
XX
XX WPI: 2003-541400/51.
XX N-PSDB; ADB61470.
XX
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
PT cancer or an immune-related disease such as multiple sclerosis, comprises
PT amino acid substitutions in the native sequence of the Apo-2 ligand.
XX
XX Claim 1; Fig 1; 92pp; English.
XX
XX The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide having a sequence that differs from the native sequence
CC having 281 amino acids given in specification. The Apo-2 ligand variant
CC polypeptide is selected from a polypeptide having substitutions at
CC residue positions identified from x-ray crystal structure of the
CC DR5-Apo2L complex. The polypeptide having the substitutions made at
CC residue position(s) selected from 20 positions such as S96C, S101C,
CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, S153C, R170C,
CC R170K, R170S, K179C, D234C, R255C, E263C, H264C, such that the
CC residue position is, outside of the receptor contact region of the
CC DR5 Apo2L complex, and displays high solvent accessibility in the crystal
CC structure of the DR5 Apo2L complex. The Apo-2 ligand variant polypeptide
CC and further compositions have the following activities: cytostatic,
CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
CC inducing apoptosis in mammalian cells, by exposing mammalian cells
CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
CC immune-related disease (such as arthritis or multiple sclerosis) in a
CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the native human Apo-2 ligand protein of
CC the invention.
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 281; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKQNISPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKQNISPLVRERGQ 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180
QY 181 FYIYISQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPPDILLMKSGARNCSKDAEYGLY 240

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Db 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
RESULT 37
ADC35202
ID ADC35202 standard; protein; 281 AA.
XX ADC35202;
AC ADC35202;
XX 18-DEC-2003 (first entry)
DT Human TNF ligand family member #10.
DE human; tumour necrosis factor; TNF ligand; endokine alpha;
XX excessive bone resorption disorder; osteoporosis; Paget's disease;
KW arterial calcification.
KW Homo sapiens.
OS Homo sapiens.
XX US2003100074-A1.
PN 29-MAY-2003.
XX 15-AUG-2002; 2002US-00218547.
PF 16-AUG-2001; 2001US-0312542P.
PR 30-OCT-2001; 2001US-0330761P.
XX (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (NARD/) NARDELLI B.
XX Yu G, Ni J, Rosen CA, Nardelli B;
PI WPI; 2003-696072/66.
DR N-PSDB; ADC35201.
XX New Endokine alpha gene useful for preparing a composition for treating a
PT disease associated with excessive or insufficient bone resorption e.g.,
PT osteoporosis, Paget's disease or arterial calcification.
XX Disclosure; SEQ ID NO 20; 145pp; English.
PS The invention relates to an isolated nucleic acid molecule encoding a
XX tumour necrosis factor family ligand. A composition comprising the
CC isolated antibody or its fragment is used for treating an individual in
CC need of decreased level of endokine alpha activity. The endokine alpha
CC polypeptide present in a heterotrimeric complex is used for treating an
CC individual having a disorder associated with excessive bone resorption,
CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an
CC individual having a disorder associated with insufficient bone resorption
CC comprises administering an endokine alpha antagonist, which is the
CC antibody that binds specifically to endokine alpha polypeptide. The
CC present sequence represents the amino acid sequence of a tumour necrosis
XX factor family ligand.
XX Sequence 281 AA;
SQ Query Match 100.0%; Score 281; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266; Indels 0; Gaps 0;
Matches 281; Conservative 0; Mismatches 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTLLQSLCAVAVYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTLLQSLCAVAVYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDESMNSPCQVQKWLVRKMLRTSEETISTVQEKQONISPLVREGRQ 120

Db 61 DDSYWDPNDESMNSPCQVQKWLVRKMLRTSEETISTVQEKQONISPLVREGRQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLRLRGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLRLRGELVIHEKG 180
QY 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
RESULT 38
ADD14080
ID ADD14080 standard; protein; 281 AA.
XX ADD14080;
AC ADD14080;
XX 01-JAN-2004 (first entry)
DT Human src biomarker polypeptide SEQ ID NO:269.
XX predictor set; protein tyrosine kinase activity modulator;
DE protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
KW gene therapy; drug sensitivity; genetic profile; cancer; human.
KW Homo sapiens.
OS Homo sapiens.
XX WO2003062395-A2.
PN 31-JUL-2003.
XX 17-JAN-2003; 2003WO-US001981.
PF 18-JAN-2002; 2002US-0350061P.
PR (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Huang P, Fairchild CR, Lee FY, Shaw P;
PI WPI; 2003-636735/60.
DR N-PSDB; ADD14676.
XX New polynucleotides and polypeptides for predicting the activity of
PT compounds that interact with protein tyrosine kinases and/or protein
PT tyrosine kinase pathways.
XX Claim 10; SEQ ID NO 269; 139pp; English.
XX The present invention describes a predictor set comprising a plurality of
CC polynucleotides or polypeptides whose expression pattern is predictive of
CC the response of cells to treatment with a compound that modulates protein
CC tyrosine kinase activity or members of the protein tyrosine kinase
CC pathway. Also described: (1) predicting whether a compound is capable of
CC modulating the activity of cells, comprising obtaining a sample of cells,
CC determining whether the cells express a plurality of markers, and
CC correlating the expression of the markers to the compound's ability to
CC modulate the activity of the cells; (2) a plurality of cell lines for
CC identifying polynucleotides and polypeptides whose expression levels
CC correlate with compound sensitivity or resistance of cells associated
CC with a disease state; and (3) identifying polynucleotides and
CC polypeptides that predict compound sensitivity or resistance of cells
CC associated with a disease state, comprising subjecting the plurality of
CC cell lines to one or more compounds, analysing the expression pattern of
CC a microarray of polynucleotides or polypeptides, and selecting
CC polynucleotides or polypeptides that predict the sensitivity or
CC resistance of cells associated with a disease state by using the
CC expression pattern of the microarray. The polynucleotides and
CC polypeptides have cytostatic activities, and can be used in gene therapy.
CC The polynucleotides and polypeptides are useful in predicting the

CC activity of compounds that interact with protein tyrosine kinases and/or
 CC protein tyrosine kinase pathways. These may be used in determining drug
 CC sensitivity in patients to allow the development of individualized
 CC genetic profiles which aid in treating diseases and disorders (e.g.
 CC cancer) based on patient response at a molecular level. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNISPVRERGQ 120
 DB 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNISPVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
 QY 181 FYIYSQTYFRQEEIKENTKNDKQVQYIYKYTSYVYFTNELKQMDKYSGIACFLKE 240
 DB 181 FYIYSQTYFRQEEIKENTKNDKQVQYIYKYTSYVYFTNELKQMDKYSGIACFLKE 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 39
 ADD19010
 ID ADD19010 standard; protein; 281 AA.
 AC
 XX ADD19010;
 DT 15-JAN-2004 (first entry)
 XX
 DE Human disease related protein SeqID499.
 XX
 KW human; disease state; cystostatic; antiinflammatory; ophthalmological;
 KW antiarteriosclerotic; vulnary; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transportation; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing.
 XX
 OS Homo sapiens.
 XX
 PN WO2003018621-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 23-AUG-2002; 2002WO-GB003892.
 XX
 PR 23-AUG-2001; 2001GB-00020558.
 PR 05-OCT-2001; 2001GB-00024037.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 XX
 DR WPI; 2003-290046/28.
 DR N-PSDB; ADD19011.
 XX
 PT New substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion

PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.
 XX
 PS Claim 25; SEQ ID NO 499; 424pp; English.
 XX
 CC This invention relates to novel human genes and gene product which are
 CC implicated in certain disease states. Compounds which modulate the
 CC proteins of the invention may have cystostatic, antiinflammatory, the
 CC ophthalmological, antiarteriosclerotic or vulnary activities. The
 CC sequences of the invention may be useful for gene therapy. The invention
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
 CC erythropoiesis, or the biological response to hypoxia conditions
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transportation, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein of the invention.
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNISPVRERGQ 120
 DB 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNISPVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
 QY 181 FYIYSQTYFRQEEIKENTKNDKQVQYIYKYTSYVYFTNELKQMDKYSGIACFLKE 240
 DB 181 FYIYSQTYFRQEEIKENTKNDKQVQYIYKYTSYVYFTNELKQMDKYSGIACFLKE 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 40
 ABW02276
 ID ABW02276 standard; protein; 281 AA.
 AC
 XX ABW02276;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human TRAIL protein.
 XX
 KW Gastrointestinal tract disorder; tumour necrosis factor; TNF; DR3; TR6;
 KW TNF-gamma-beta protein; inflammatory bowel disease; Crohn's disease;
 KW ulcerative colitis; TRAIL; human.
 XX
 OS Homo sapiens.
 XX
 PN US2003198640-A1.
 XX
 PD 23-OCT-2003.
 XX
 PF 06-DEC-2002; 2002US-00310793.
 XX
 PR 07-NOV-1994; 94WO-US012880.
 PR 05-JUN-1995; 95US-00461246.
 PR 09-JAN-1998; 98US-00005020.
 PR 09-FEB-1998; 98US-0074047P.

PR 07-AUG-1998; 98US-00131237.
PR 08-FEB-1999; 99US-00246129.
PR 30-APR-1999; 99US-0131963P.
PR 03-MAY-1999; 99US-0132227P.
PR 13-MAY-1999; 99US-0134067P.
PR 08-FEB-2000; 2000US-0180908P.
PR 27-APR-2000; 2000US-0055929P.
PR 07-JUL-2000; 2000US-0216879P.
PR 26-MAR-2001; 2001US-0278449P.
PR 06-JUL-2001; 2001US-0089905P.
PR 24-AUG-2001; 2001US-0314381P.
PR 07-DEC-2001; 2001US-0336695P.
PR 23-AUG-2002; 2002US-00226294.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Yu G, Ni J, Rosen CA, Zhang J, Wei P;
PI WPI; 2003-852773/79.
DR N-PSDB; AAD63912.
XX
XX Use of tumor necrosis factor gamma-beta antagonists for treating or
PT ameliorating a disease or disorders of the gastrointestinal tract, e.g.
PT inflammatory bowel disease, Crohn's disease or ulcerative colitis.
XX
XX Disclosure; Page 140-141; Opp; English.
XX
XX The invention relates to methods and compositions for treating or
CC ameliorating a disease or disorder of the gastrointestinal tract. The
CC method involves administering a composition comprising tumour necrosis
CC factor (TNF)-gamma-beta and its receptors DR3 and TR6 to a person with,
CC or suspected of having the disease or disorder. The antagonist of TNF-
CC gamma-beta is useful for treating or ameliorating a gastrointestinal
CC tract disease or disorder, specifically an inflammatory bowel disease,
CC e.g. Crohn's disease or ulcerative colitis. The present sequence is human
CC TRAIL protein. This sequence is used to illustrate the method of the
CC invention
XX
XX Sequence 281 AA;
Query Match 100.0%; Score 281; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSRNSCKDAEYGLY 240
DB 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSRNSCKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
RESULT 41
ADE76953
ID ADE76953 standard; protein; 281 AA.
XX
AC ADE76953;
XX
DT 29-JAN-2004 (first entry)
XX

DE Human protein expressed in a liver disorder #32.
XX human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
KW tumour; liver; inflammatory disorder; immune response disorder;
KW high-throughput screening; differential gene expression; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003108871-A1.
XX 12-JUN-2003.
PD 30-JUL-2001; 2001US-00919039.
XX 28-JUL-2000; 2000US-0222113P.
XX (KASE/) KASER M R.
PA Kaser MR;
XX
XX WPI; 2004-031227/03.
DR N-PSDB; ADE76952.
XX
XX Composition comprising several cDNAs that are differentially expressed in
PT treated human C3A liver cell cultures, useful for treating liver
PT disorders.
XX
XX Claim 1; SEQ ID NO 118; 41pp; English.
PS
XX The invention relates to a composition comprising several cDNAs that are
CC differentially expressed in a liver disorder. The composition is useful
CC for treating liver disorder such as hyperlipidaemia, hypertension, type
CC II diabetes, tumours of the liver and disorders of the inflammatory and
CC immune response. The composition is useful for a high-throughput method
CC of screening several molecules or compounds to identify a ligand which
CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
CC high-throughput method for using a protein to screen several molecules or
CC compounds to identify at least one ligand which specifically binds the
CC protein which involves combining the protein encoded by the cDNA with
CC several of molecules or compounds under conditions to allow specific
CC binding, and detecting specific binding between the protein and a
CC molecule or compound, therefore identifying a ligand which specifically
CC binds the protein. The composition is useful for detecting and
CC quantifying differential gene expression, can be used in gene therapy, to
CC formulate prognosis and to design a treatment regimen and to monitor the
CC efficacy of treatment. The present sequence represents the amino acid
CC sequence of a protein encoded by a cDNA differentially expressed in a
CC liver disorder.
XX
XX Sequence 281 AA;
Query Match 100.0%; Score 281; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSRNSCKDAEYGLY 240
DB 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSRNSCKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
XX

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 42

ADK72311

ID ADK72311 standard; protein; 281 AA.

XX ADK72311;

AC ADK72311;

XX 06-MAY-2004 (first entry)

XX Human Apo-2 ligand with potential substitutions highlighted #4.

DE Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;

KW variant; cancer; immune system disease; arthritis; multiple sclerosis;

KW human.

XX Homo sapiens.

OS

XX

XX Key Location/Qualifiers

FT Misc-difference 189

FT /note= "wild-type Tyr may be substituted by Ala, Ser or

FT Xaa (where Xaa is encoded by an amber codon) at this

FT location in the variant referred to in claim 17"

FT Misc-difference 191

FT /note= "wild-type Arg may be substituted by Lys at this

FT location in the variant referred to in claim 17"

FT Misc-difference 193

FT /note= "wild-type Gln may be substituted by Arg at this

FT location in the variant referred to in claim 17"

FT Misc-difference 264

FT /note= "wild-type His may be substituted by Arg, Asp,

FT Asn, Ala, Pro or Thr at this location in the variant

FT referred to in claim 17"

FT Misc-difference 266

FT /note= "wild-type Ile may be substituted by Val or Leu at

FT this location in the variant referred to in claim 17"

FT Misc-difference 267

FT /note= "wild-type Asp may be substituted by Asn, Glu or

FT Gln at this location in the variant referred to in claim

FT 17"

XX

PN WO2004001009-A2.

XX

XX 31-DEC-2003.

XX

XX 23-JUN-2003; 2003WO-US019750.

XX

XX 24-JUN-2002; 2002US-0391050P.

XX (GETH) GENENTECH INC.

XX Hymowitz S, Kelley RP, Lindstrom SH;

PI WPI; 2004-082490/08.

DR

XX New Apo-2 ligand variant polypeptide, useful for preparing a composition

PT for treating cancer or immune-related disease, e.g., arthritis or

PT multiple sclerosis.

XX Claim 17; SEQ ID NO 1; 111pp; English.

PS

XX The invention relates to a novel isolated Apo-2 ligand variant

CC polypeptide, comprising a sequence that differs from the native sequence

CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having

CC one or more following amino acid substitutions at the residue positions

CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an

CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand

CC variant polypeptide. Further disclosed are a composition comprising the

CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a

CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant

CC polypeptide is useful for preparing a composition for treating cancer or

CC immune-related disease, e.g., arthritis or multiple sclerosis. The

CC current sequence represents the human Apo-2 ligand amino acid sequence.

CC Note: The variant sequence that is referred to in claim 17 may contain

CC one or more of the potential substitutions highlighted in the features

CC table for this record.

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.9e-266;

Mismatches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGKGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGKGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQKQKNISPLVRERGQ 120

DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQKQKNISPLVRERGQ 120

QY 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

DB 121 RYAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYRFPQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKRSARNSCWKDAEYGLY 240

DB 181 FYIYSQTYRFPQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKRSARNSCWKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 43

ADK72303

ID ADK72303 standard; protein; 281 AA.

XX ADK72303;

AC ADK72303;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human Apo-2 ligand with potential substitutions highlighted #1.

XX

KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;

KW variant; cancer; immune system disease; arthritis; multiple sclerosis;

KW human.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Misc-difference 96

FT /note= "wild-type ser may be substituted for Cys at this

FT location in the variant referred to in claim 1"

FT Misc-difference 101

FT /note= "wild-type ser may be substituted for Cys at this

FT location in the variant referred to in claim 1"

FT Misc-difference 111

FT /note= "wild-type ser may be substituted for Cys at this

FT location in the variant referred to in claim 1"

FT Misc-difference 170

FT /note= "wild-type Arg may be substituted for Cys at this

FT location in the variant referred to in claim 1"

FT Misc-difference 179

FT /note= "wild-type Lys may be substituted for Cys at this

FT location in the variant referred to in claim 1"

XX WO2004001009-A2.

XX 31-DEC-2003.

XX 23-JUN-2003; 2003WO-US019750.

XX 24-JUN-2002; 2002US-0391050P.

XX

```
PA (GETH ) GENENTECH INC.
XX
PI Hymowitz S, Kelley RF, Lindstrom SH;
XX
DR WPI; 2004-082490/08.
XX
PT New Apo-2 ligand variant polypeptide, useful for preparing a composition
PT for treating cancer or immune-related disease, e.g., arthritis or
PT multiple sclerosis.
XX
XX
PS Claim 1; SEQ ID NO 1; 111pp; English.
XX
CC The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide, comprising a sequence that differs from the native sequence
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having
CC one or more following amino acid substitutions at the residue positions
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
CC variant polypeptide. Further disclosed are a composition comprising the
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant
CC polypeptide is useful for preparing a composition for treating cancer or
CC immune-related disease, e.g., arthritis or multiple sclerosis. The
CC current sequence represents the human Apo-2 ligand amino acid sequence.
CC Note: The variant sequence that is referred to in claim 1 may contain one
CC or more of the potential substitutions highlighted in the features table
CC for this record.
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVKMLRTSEETISTVQSKQNI SPLVRERGPQ 120
DB 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVKMLRTSEETISTVQSKQNI SPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSRNSCWKDAEYGLY 240
DB 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSRNSCWKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 44
ADK72304
ID ADK72304 standard; protein; 281 AA.
XX
AC ADK72304;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Human Apo-2 ligand with potential substitutions highlighted #2.
XX
KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;
KW human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 189

/note= "wild-type Tyr may be substituted by Ala at this
location in the variant referred to in claim 2"
FT Misc-difference 193
/note= "wild-type Gln may be substituted by Arg, Ser,
Thr, Val or Lys at this location in the variant referred
to in claim 2"
FT Misc-difference 199
/note= "wild-type Asn may be substituted by Gly, Lys, Val
or Arg at this location in the variant referred to in
claim 2"
FT Misc-difference 201
/note= "wild-type Lys may be substituted by His, Ala,
Arg, Gly, Thr or Ser at this location in the variant
referred to in claim 2"
FT
FT WO2004001009-A2.
XX
XX 31-DEC-2003.
XX
XX 23-JUN-2003; 2003WO-US019750.
XX
XX 24-JUN-2002; 2002US-0391050P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Hymowitz S, Kelley RF, Lindstrom SH;
XX
XX WPI; 2004-082490/08.
XX
XX New Apo-2 ligand variant polypeptide, useful for preparing a composition
for treating cancer or immune-related disease, e.g., arthritis or
multiple sclerosis.
XX
XX Claim 2; SEQ ID NO 1; 111pp; English.
XX
CC The invention relates to a novel isolated Apo-2 ligand variant
polypeptide, comprising a sequence that differs from the native sequence
Apo-2 ligand polypeptide sequence comprising 282 amino acids and having
one or more following amino acid substitutions at the residue positions
comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an
isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
variant polypeptide. Further disclosed are a composition comprising the
Apo-2 ligand variant polypeptide, a method of treating cancer, and a
method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant
polypeptide is useful for preparing a composition for treating cancer or
immune-related disease, e.g., arthritis or multiple sclerosis. The
current sequence represents the human Apo-2 ligand amino acid sequence.
Note: The variant sequence that is referred to in claim 2 may contain one
or more of the potential substitutions highlighted in the features table
for this record.
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVKMLRTSEETISTVQSKQNI SPLVRERGPQ 120
DB 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVKMLRTSEETISTVQSKQNI SPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSRNSCWKDAEYGLY 240
DB 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSRNSCWKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281
```

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281

RESULT 45
 ADK72296
 ID ADK72296 standard; protein; 281 AA.
 XX
 AC ADK72296;
 XX
 DT 06-MAY-2004 (first entry)
 DE Human wild-type Apo-2 ligand, seq id 1.
 DE
 XX Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;
 KW variant; cancer; immune system disease; arthritis; multiple sclerosis;
 KW human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 119
 FT /note= "Encoded by CCN"
 XX
 PN WO2004001009-A2.
 XX
 PD 31-DEC-2003.
 XX
 PF 23-JUN-2003; 2003WO-US019750.
 XX
 PR 24-JUN-2002; 2002US-0391050P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Hymowitz S, Kelley RF, Lindstrom SH;
 XX
 DR WPI; 2004-082490/08.
 DR N-PSDB; ADK72297.
 XX
 PT New Apo-2 ligand variant polypeptide, useful for preparing a composition
 PT for treating cancer or immune-related disease, e.g., arthritis or
 PT multiple sclerosis.
 XX
 PS Claim 1; SEQ ID NO 1; 111pp; English.
 XX
 CC The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide, comprising a sequence that differs from the native sequence
 CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having
 CC one or more following amino acid substitutions at the residue positions
 CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an
 CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
 CC variant polypeptide. Further disclosed are a composition comprising the
 CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a
 CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant
 CC polypeptide is useful for preparing a composition for treating cancer or
 CC immune-related disease, e.g., arthritis or multiple sclerosis. The
 CC current sequence represents the wild-type human Apo-2 ligand amino acid
 CC sequence.
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVIVITVLQSLCVAVTVYFTNELKQMDKYSKGIACFLKE 60
 Db 1 MAMMEVQGGPSLQGTCLVIVITVLQSLCVAVTVYFTNELKQMDKYSKGIACFLKE 60
 QY 61 DSDYDPNDEESMNSPCWQVKQRLVRKMLRTSEETISTVQEKQQNISPVLVRGPGQ 120
 Db 61 DSDYDPNDEESMNSPCWQVKQRLVRKMLRTSEETISTVQEKQQNISPVLVRGPGQ 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHKG 180
 Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHKG 180
 QY 181 FYIYISQTYFRFQBEIKENTKNDKQMVQIYKYTSYPPDPILLMKSGARNSCWSDAEYGLY 240
 Db 181 FYIYISQTYFRFQBEIKENTKNDKQMVQIYKYTSYPPDPILLMKSGARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281

RESULT 46
 ADK72310
 ID ADK72310 standard; protein; 281 AA.
 XX
 AC ADK72310;
 XX
 DT 06-MAY-2004 (first entry)
 DE Human Apo-2 ligand with potential substitutions highlighted #3.
 DE
 XX Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;
 KW variant; cancer; immune system disease; arthritis; multiple sclerosis;
 KW human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 189
 FT /note= "wild-type Tyr may be substituted by Ala, Ser, Gln
 FT or Gly at this location in the variant referred to in
 FT claim 10"
 FT
 FT Misc-difference 191
 FT /note= "wild-type Arg may be substituted by Lys or Arg at
 FT this location in the variant referred to in claim 10"
 FT
 FT Misc-difference 193
 FT /note= "wild-type Gln may be substituted by Lys, Arg or
 FT Thr at this location in the variant referred to in claim
 FT 10"
 FT
 FT Misc-difference 264
 FT /note= "wild-type His may be substituted by Ala, His,
 FT Gly, Gln, Asp, Arg, Pro, Ser, Glu, Asn or Lys at this
 FT location in the variant referred to in claim 10"
 FT
 FT Misc-difference 266
 FT /note= "wild-type Ile may be substituted by Leu, Met or
 FT Val at this location in the variant referred to in claim
 FT 10"
 FT
 FT Misc-difference 267
 FT /note= "wild-type Asp may be substituted by Ser, Glu,
 FT Gln, Asp or Asn at this location in the variant referred
 FT to in claim 10"
 FT
 FT Misc-difference 269
 FT /note= "wild-type Asp may be substituted by Ser, Asn,
 FT Asp, Ala, Arg or Glu at this location in the variant
 FT referred to in claim 10"
 XX
 PN WO2004001009-A2.
 XX
 PD 31-DEC-2003.
 XX
 PF 23-JUN-2003; 2003WO-US019750.
 XX
 PR 24-JUN-2002; 2002US-0391050P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Hymowitz S, Kelley RF, Lindstrom SH;
 XX
 DR WPI; 2004-082490/08.
 XX

PT New Apo-2 ligand variant polypeptide, useful for preparing a composition
PT for treating cancer or immune-related disease, e.g., arthritis or
XX multiple sclerosis.
PS Claim 10; SEQ ID NO 1; 111pp; English.
XX
CC The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide, comprising a sequence that differs from the native sequence
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having
CC one or more following amino acid substitutions at the residue positions
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
CC variant polypeptide. Further disclosed are a composition comprising the
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant
CC polypeptide is useful for preparing a composition for treating cancer or
CC immune-related disease, e.g., arthritis or multiple sclerosis. The
CC current sequence represents the human Apo-2 ligand amino acid sequence.
CC Note: The variant sequence that is referred to in claim 10 may contain
CC one or more of the potential substitutions highlighted in the features
XX table for this record.
SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVITFTVLLQSLCVAVTVYFTNKLQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVITFTVLLQSLCVAVTVYFTNKLQMDKYSGIACFLKE 60
QY 61 DDSYDNPNDDESMNSPCQVKWQLRQLVKMTLTSEETISTVQKQKQNSPLVRERGQ 120
DB 61 DDSYDNPNDDESMNSPCQVKWQLRQLVKMTLTSEETISTVQKQKQNSPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKDKQWQYIYKYTSYDPDILLMKSNCSKDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKDKQWQYIYKYTSYDPDILLMKSNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFVLG 281

RESULT 47
ID ADJ63976
XX ADJ63976 standard; protein; 281 AA.
AC ADJ63976;
XX
XX 20-MAY-2004 (first entry)
XX
DE Human apoptosis inducing molecule 1, AIM-1.
XX
KW Human; apoptosis inducing molecule 1; AIM-1; apoptosis;
KW autoimmune disease; graft versus host disease; lymphadenopathy;
KW immunosuppressive; vasotropic; cytostatic; peripheral tolerance;
KW cell activation; cell proliferation; immune regulation;
KW inflammatory response; systemic lupus erythematosus;
KW immunoproliferative disease; neoplasm; tumour; restenosis.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..38
FT Peptide /note= "signal peptide"
FT Protein 39..281
FT /label= Mature_AIM_1
FT

FT
XX
PN US2004038347-A1. /note= "Claimed in claim 1"
XX
PD 26-FEB-2004.
XX
XX 16-SEP-2003; 2003US-00662429.
PF
XX 14-MAR-1996; 96US-0013405P.
PR
XX 13-MAR-1997; 97US-00816981.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Ruben SM;
PI
XX WPI; 2004-203230/19.
DR N-PSDB; ADJ63975.
XX
XX Novel apoptosis inducing molecule polypeptide that induces apoptosis of
PT cell line derived from pathological tissue and induces apoptosis of T
PT cells, useful for treating lymphadenopathy, autoimmune diseases and graft
PT versus host disease.
XX
PS Claim 1; SEQ ID NO 2; 36pp; English.
XX
CC The invention relates to apoptosis inducing molecule-I protein (AIM-I)
CC comprising sequence that is 70 % identical to ADJ63976 or its mature form
CC where the polypeptide binds antibody specific to AIM-1, induces apoptosis
CC of cell line derived from pathological tissue and induces apoptosis of T
CC cells. Also included are a composition comprising AIM-1 and a carrier,
CC AIM-1 produced by a process involving expressing in a host cell a nucleic
CC acid that encodes the protein so as to produce the protein (where the
CC nucleic acid is chosen from a polynucleotide encoding AIM-1, mature AIM-
CC 1, mature AIM-1 except for 1-5 or 5-10 conservative amino acid
CC substitutions, the amino acid sequence encoded by human cDNA contained in
CC ATCC deposit No. 97448, and a polynucleotide that is complementary to
CC polynucleotide which hybridises at 60degreesC in a hybridisation buffer
CC consisting of 0.5 X SSC (Saline-Sodium Citrate) and 0.1 % sodium dodecyl
CC sulphate (SDS) to a polynucleotide chosen from polynucleotide encoding
CC mature AIM-1, and a polynucleotide encoding amino acid sequence encoded
CC by human cDNA contained in ATCC deposit No. 97448, where the
CC polynucleotide encodes a polypeptide that has the same biological
CC activity as described above). AIM-1 is useful for treating
CC lymphadenopathy, autoimmune diseases, graft versus host disease, for
CC stimulating peripheral tolerance, destroying pathologic transformed cell
CC lines, mediating cell activation and proliferation. AIM-1 proteins are
CC functionally linked as primary mediators of immune regulation and
CC inflammatory response, are useful for diagnosis and treatment of
CC disorders of cells, tissues and organisms. AIM-1 is useful as research
CC tool in elucidating biology of autoimmune disorders including systemic
CC lupus erythematosus, immunoproliferative disease lymphadenopathy and is
CC useful for inhibiting neoplasia such as tumour cell growth. AIM-1 is also
CC useful to treat diseases which required growth promotion activity e.g.,
CC restenosis. AIM-1 is useful for assessing AIM-I binding capacity of its
CC binding molecules such as receptor molecules. The present sequence
XX represents AIM-1.
SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVITFTVLLQSLCVAVTVYFTNKLQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVITFTVLLQSLCVAVTVYFTNKLQMDKYSGIACFLKE 60
QY 61 DDSYDNPNDDESMNSPCQVKWQLRQLVKMTLTSEETISTVQKQKQNSPLVRERGQ 120
DB 61 DDSYDNPNDDESMNSPCQVKWQLRQLVKMTLTSEETISTVQKQKQNSPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Db 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSNRSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSNRSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 48
 ADL71816
 ID ADL71816 standard; protein; 281 AA.
 AC ADL71816;
 DT 03-JUN-2004 (first entry)
 DE Human apoptosis inducing molecule-I (AIM-I) protein.
 XX
 KW Apoptosis inducing molecule-I; AIM-I; cell activation;
 KW cell differentiation; apoptosis; autoimmune disease;
 KW graft-versus-host disease; lymphadenopathy; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004047864-A1.
 XX
 PD 11-MAR-2004.
 XX
 PF 16-SEP-2003; 2003US-00662431.
 XX
 PR 14-MAR-1996; 96US-0013405P.
 PR 13-MAR-1997; 97US-00816981.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM;
 XX
 DR WPI; 2004-226168/21.
 DR N-PSDB; ADL71815.
 XX
 PT New antibodies specific to apoptosis inducing molecule I polypeptides
 PT useful in research, biological, diagnostic, clinical or therapeutic
 PT applications, such as in the treatment of autoimmune diseases or graft-
 PT versus-host disease.
 XX
 PS Claim 1; SEQ ID NO 2; 36pp; English.
 XX
 CC The invention relates to antibodies specific to apoptosis inducing
 CC molecule-I (AIM-I) polypeptides. The invention is useful in research,
 CC biological, diagnostic, clinical or therapeutic applications. It is also
 CC used for modulating activation and differentiation of cells, both
 CC normally and in disease states, or for mediating apoptosis and preventing
 CC or treating autoimmune diseases, graft-versus-host disease or
 CC lymphadenopathy. The invention is also useful in gene therapy. The
 CC present sequence is human AIM-I protein.
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTLVLQSLCVAVTVYFTNKLQMDKYKSGIACFLKE 60
 Db 1 MAMMEVQGGPSLGQTCVLIVFTLVLQSLCVAVTVYFTNKLQMDKYKSGIACFLKE 60
 QY 61 DDSYWDPNDESNWPCWQVKQLRQVRKMLRITSEETISTVQEQQNISPLVRGPGQ 120
 Db 61 DDSYWDPNDESNWPCWQVKQLRQVRKMLRITSEETISTVQEQQNISPLVRGPGQ 120

QY 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
 Db 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSNRSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSNRSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 49
 ADK15498
 ID ADK15498 standard; protein; 281 AA.
 AC ADK15498;
 DT 03-JUN-2004 (first entry)
 DE Human TRAIL protein.
 XX
 KW Human; TRAIL; TNF related apoptosis inducing ligand; apoptosis;
 KW cytostatic; virucide; tumour necrosis factor; Jurkat cell; cancer;
 KW programmed cell death; leukaemia; colorectal cancer; viral infection;
 KW vaccine.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..18 /note= "Cytoplasmic domain"
 FT Domain 19..38 /note= "Transmembrane domain"
 FT Domain 39..281 /note= "Extracellular domain claimed in claim 4"
 FT Region 95..281 /note= "Claimed in claim 7"
 FT
 XX
 PN US2004052788-A1.
 XX
 PD 18-MAR-2004.
 XX
 PF 02-SEP-2003; 2003US-00652244.
 XX
 PR 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548368.
 PR 25-JUN-1996; 96US-00670354.
 PR 26-MAR-1998; 98US-00048641.
 PR 10-NOV-1998; 98US-00190046.
 PR 26-MAY-1999; 99US-00320424.
 PR 27-FEB-2001; 2001US-00796581.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Wiley SR, Goodwin RG;
 XX
 DR WPI; 2004-238577/22.
 DR N-PSDB; ADK15497.
 XX
 PT New tumor necrosis factor related apoptosis inducing ligand polypeptides,
 PT useful in studies of apoptosis, in regulating programmed cell death, or
 PT for treating leukemia, cancer (e.g. colorectal cancer) or viral
 PT infections.
 XX
 PS Claim 2; SEQ ID NO 2; 42pp; English.
 XX
 CC The invention relates to a new purified tumour necrosis factor related
 CC apoptosis inducing ligand (TRAIL) polypeptide comprising an amino acid
 CC sequence that is at least 90% identical to human TRAIL (ADK15498) or
 CC mouse TRAIL (ADK15502). The TRAIL polypeptide induces apoptosis of Jurkat
 CC cells. Also included are a purified human TRAIL polypeptide encoded by

CC the cDNA insert of the recombinant vector deposited in strain ATCC 69849
 CC (or a fragment of human TRAIL protein of SEQ ID NO: 2 that induces
 CC apoptosis of Jurkat cells), a fusion protein comprising a leucine zipper
 CC peptide and a soluble TRAIL polypeptide (comprising the extracellular
 CC domain) and a leucine zipper comprising ADK15510-ADK15513, an oligomer
 CC comprising at least two soluble TRAIL polypeptides (or at least two
 CC fusion proteins defined above), an antibody that specifically binds a
 CC TRAIL protein above and a method of inducing death of cancer cells (by
 CC contacting TRAIL-sensitive cancer cells with a TRAIL polypeptide or with
 CC an oligomer defined above). The TRAIL polypeptide is useful in studies of
 CC apoptosis, in regulating programmed cell death, for treating leukaemia,
 CC cancer (e.g. colorectal cancer) or viral infections, or in purifying
 CC leukaemic cells or a desired cell surface antigen which can be used in
 CC vaccine development. The TRAIL polypeptide may also be used in developing
 CC treatments for any disorder mediated by defective or insufficient amounts
 CC of TRAIL. The present sequence represents human TRAIL.

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
 DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTYSPDPILLMKARSNCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTYSPDPILLMKARSNCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 50
 ADN07587

ID ADN07587 standard; protein; 281 AA.

XX AC ADN07587;

XX 17-JUN-2004 (first entry)

XX DE Human apoptosis inducing molecule-1 protein.

XX Apoptosis inducing molecule I; AIM-I; therapeutic; autoimmune disorder;
 KW systemic lupus erythematosus;
 KW immunoproliferative disease lymphadenopathy; IPL;
 KW angioimmunoproliferative lymphadenopathy; AIL; rheumatoid arthritis;
 KW diabetes; multiple sclerosis; graft versus host disease;
 KW lymphoproliferative disease; lymphadenopathy; neoplasia;
 KW tumour cell growth; restenosis; haematopoiesis;
 KW chromosome identification; pancreatic tumour; endometrial tumour;
 KW T-cell lymphoma; gene therapy; human.

XX OS Homo sapiens.

XX PN US2004048340-A1.

XX PD 11-MAR-2004.

XX PF 16-SEP-2003; 2003US-00662430.

XX PR 14-MAR-1996; 96US-0013405P.

PR 13-MAR-1997; 97US-00816981.

XX (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM;

XX WIPI; 2004-238497/22.

XX DR N-PSDB; ADN07586.

XX Novel human apoptosis inducing molecule I useful for treating
 PT lymphadenopathy, systemic lupus erythematosus, rheumatoid arthritis and
 PT multiple sclerosis.

PS Claim 1; SEQ ID NO 2; 35pp; English.

CC The present invention relates to apoptosis inducing molecule I (AIM-I)
 CC polypeptide and the encoding polynucleotide useful in biological, in
 CC diagnostic, clinical and therapeutic arts. The invention is useful in
 CC treating autoimmune disorders such as systemic lupus erythematosus,
 CC immunoproliferative disease lymphadenopathy (IPL),
 CC angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
 CC diabetes and multiple sclerosis, graft versus host disease,
 CC lymphoproliferative disease such as lymphadenopathy, in inhibiting
 CC neoplasia such as tumour cell growth, in treating restenosis and
 CC regulating haematopoiesis in endothelial cell development. The invention
 CC is useful in chromosome identification and as a diagnostic marker for
 CC determining expression of AIM-I polypeptide in tumour cell lines
 CC including pancreatic tumour, endometrial tumour and T-cell lymphoma. The
 CC invention is also useful in gene therapy. The present sequence is human
 CC apoptosis inducing molecule I (AIM-I) protein.

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.9e-266;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120

DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTYSPDPILLMKARSNCWSKDAEYGLY 240

DB 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTYSPDPILLMKARSNCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 51

ADRI4209

ID ADRI4209 standard; protein; 281 AA.

XX AC ADRI4209;

XX DT 21-OCT-2004 (first entry)

XX DE Human NF-kappaB pathway-associated protein SeqID210.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiaesthetic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnery; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;

KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; human.
 XX Homo sapiens.
 OS
 XX WO2004065577-A2.
 PN
 XX
 PD
 XX
 XX
 PF 13-JAN-2004; 2004WO-US000798.
 PR
 XX 14-JAN-2003; 2003US-0440068P.
 PR 12-MAY-2003; 2003US-0469757P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX
 XX Nadler SG, Neubauer MG, Feder JN, Carman J;
 PI
 DR WPI; 2004-562168/54.
 DR N-PSDB; ADR14208.
 DR
 XX New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.
 PT
 XX
 XX Claim 6; SEQ ID NO 210; 237pp; English.
 PS
 XX This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an anti-inflammatory,
 CC cytostatic, hepatotropic, virucide, antiarthritic, anti-rheumatic,
 CC gastrointestinal-Cen, antiasthmatic, antiarteriosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnary activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.
 XX
 XX Sequence 281 AA;
 SQ
 Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTYVFTNKLKQMDKYKSGIACFLKE 60
 |||||
 61 DDYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNNISPLVREGPQ 120
 |||||
 61 DDYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNNISPLVREGPQ 120
 |||||
 121 RVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLNRLNGELVTHEKG 180
 |||||
 121 RVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLNRLNGELVTHEKG 180
 |||||
 181 FYYIYSQYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSGARNSCWKDAEYGLY 240
 |||||
 181 FYYIYSQYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSGARNSCWKDAEYGLY 240
 |||||
 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
 |||||
 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
 |||||
 RESULT 52
 ADK82215
 ID ADK82215 standard; protein; 281 AA.
 XX
 AC ADK82215;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human TRAIL amino acid sequence SEQ ID NO:66.
 XX
 KW antibody; VH domain; VL domain; TR4 binding antibody; TRAIL receptor;
 KW haematological cancer; cytostatic; immunotherapy; Non-Hodgkin's lymphoma;
 KW chronic myelogenous lymphoma; multiple myeloma;
 KW chronic lymphocytic leukaemia; scFv; human; TRAIL;
 KW TNF-related apoptosis-inducing ligand.
 XX
 OS Homo sapiens.
 XX
 PN WO2004016753-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 15-AUG-2003; 2003WO-US025457.
 XX
 PR 15-AUG-2002; 2002US-0403382P.
 PR 13-NOV-2002; 2002US-0425730P.
 PR 06-MAY-2003; 2003US-0468050P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Salcedo T, Ruben SM, Rosen CA, Albert VA;
 PI WPI; 2004-203784/19.
 XX
 DR
 XX
 PT Use of an antibody or its fragment the specifically binds to TR4, for the
 PT preparation of a pharmaceutical composition for treating or preventing
 PT hematological cancer, e.g. Non-Hodgkin's lymphoma, multiple myeloma or
 PT leukemia.
 XX
 PS Disclosure; SEQ ID NO 66; 353pp; English.
 XX
 CC The present invention describes an antibody or its fragment comprising a
 CC VH and VL domain that is at least 80% identical to a VH and a VL domain
 CC of any of the 14 sequences given in SEQ ID NO:43 to 56, or a VH and a VL
 CC domain of an antibody expressed by any one of the cell lines contained in
 CC American Type Culture Collection (ATCC) Deposit numbers PTA-3571, PTA-
 CC 3570 and PTA-3675, where the antibody specifically binds TR4 (TRAIL
 CC receptor). Also described is a pharmaceutical composition for treating or
 CC preventing haematological cancer, comprising the antibody or its fragment
 CC and a member selected from ibritumomab tiuxetan, imatinib mesylate,
 CC bortezomib, and a smac peptide or polypeptide. The antibody has
 CC cytostatic activity, and can be used in immunotherapy. The antibody or
 CC its fragment can be used for the preparation of a pharmaceutical
 CC composition for treating or preventing haematological cancer, e.g. Non-

Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTYVFTNKLKQMDKYKSGIACFLKE 60
 |||||

```
CC Hodgkin's lymphoma, chronic myelogenous lymphoma, multiple myeloma, or
CC chronic lymphocytic leukaemia. The present sequence represents human
CC tumour necrosis factor (TNF) related apoptosis-inducing ligand (TRAIL),
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 53
ADS88000
ID ADS88000 standard; protein; 281 AA.
AC ADS88000;
XX
DT 18-NOV-2004 (first entry)
DE Tumour treatment-related human protein sequence SeqID36.
XX
KW tumour inhibition; tumour treatment; metastasis; infectious lesion;
KW antigen presenting cell; immunostimulatory cytokine; cytostatic;
KW vulnery; immunomodulator; melanoma; hepatoma; adenocarcinoma;
KW colorectal cancer; basal cell cancer; oral cancer; nasopharyngeal cancer;
KW laryngeal cancer; bladder cancer; head cancer; neck cancer;
KW renal cell cancer; pancreatic cancer; pulmonary cancer; cervical cancer;
KW ovarian cancer; oesophageal cancer; gastric cancer; prostate cancer;
KW testicular cancer; breast cancer; human.
XX
OS Homo sapiens.
XX
PN WO2004034995-A2.
XX
PD 29-APR-2004.
XX
PF 15-OCT-2003; 2003WO-US032827.
XX
PR 15-OCT-2002; 2002US-0418665P.
XX
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Lotze MT, Tahara H;
XX
DR WPI; 2004-365083/34.
DR N-PSDB; ADS87999.
XX
PT Inhibiting or treating a tumor, metastasis or infectious lesion comprises
PT administering into or near site of a tumor or infectious lesion an
PT antigen presenting cell and an immunostimulatory cytokine or a nucleic
PT acid encoding the cytokine.
XX
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PS Disclosure; SEQ ID NO 36; 169pp; English.
XX
CC This invention relates to a novel method of inhibiting or treating a
CC tumour, metastasis or infectious lesion in a subject which comprises
CC administering into or near a site of a tumour or infectious lesion in a
CC subject an antigen presenting cell and an immunostimulatory cytokine or a
CC nucleic acid encoding the cytokine. The invention may be useful for the
CC production of compounds with a cytostatic or vulnerary activity acting as
CC immunomodulators. The method is useful in inhibiting or treating a
CC tumour, metastasis or infectious lesion in a subject, where the size of
CC the tumour, metastasis (where number is also decreased) or infectious
CC lesion is decreased. The tumour is selected from melanoma, hepatoma,
CC adenocarcinoma, colorectal cancer, basal cell cancer, oral cancer,
CC nasopharyngeal cancer, laryngeal cancer, bladder cancer, head and neck
CC cancer, renal cell cancer, pancreatic cancer, pulmonary cancer, cervical
CC cancer, ovarian cancer, oesophageal cancer, gastric cancer, prostate
CC cancer, testicular cancer and breast cancer. The present sequence is that
CC of a protein which is related to the invention.
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 54
AB084415
ID AB084415 standard; protein; 281 AA.
XX
AC AB084415;
XX
DT 18-NOV-2004 (first entry)
DE Human cancer-associated protein HP7-053.3.
XX
KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;
KW lymphoma; CAP.
XX
OS Homo sapiens.
XX
PN WO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
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XX (SAGR-) SAGRES DISCOVERY INC.
 XX Morris DW, Morris DW, Malandro MS;
 XX WPI: 2004-652914/63.
 XX N-PSDB; ABD32555.
 XX New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX claim 18; seqid 36; 310pp; English.
 XX The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC a CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukaemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a human CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIVITVLQSLCVAVTVYFTNELKQMDKYSGKGIACFLKE 60
 DB |||||
 QY 1 MAMMEVGGPSLGQTCVLIVITVLQSLCVAVTVYFTNELKQMDKYSGKGIACFLKE 60
 DB |||||
 QY 61 DSDYNDPNDDESMNSPCWQVKQLRQLVKRMILRTSEETISTVQEKQKINISPLVREGRGPQ 120
 DB |||||
 QY 61 DSDYNDPNDDESMNSPCWQVKQLRQLVKRMILRTSEETISTVQEKQKINISPLVREGRGPQ 120
 DB |||||
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNLHRLNRELVIHEKG 180
 DB |||||
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNLHRLNRELVIHEKG 180
 DB |||||
 QY 181 FYIYISQTYFRQEEIKENTKDKQWQVIYKYTSYDPDILLMKSNRNSCWKDAEYGLY 240
 DB |||||
 QY 181 FYIYISQTYFRQEEIKENTKDKQWQVIYKYTSYDPDILLMKSNRNSCWKDAEYGLY 240
 DB |||||
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
 DB |||||
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
 DB |||||

RESULT 55
 ADP23388
 ID ADP23388 standard; protein; 281 AA.
 XX AC ADP23388;
 XX DT 18-NOV-2004 (first entry)
 XX DE PRO polypeptide SEQ ID NO:566.
 XX KW PRO: antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipsoiatic; antiallergic;
 KW antiaschmatic; hepatotropic; respiratory; gene therapy; immune system.
 XX Unidentified.
 XX WO2004041170-A2.
 XX PD 21-MAY-2004.
 XX PF 30-OCT-2003; 2003WO-US034312.
 XX PR 01-NOV-2002; 2002US-0423394P.
 XX (GETH) GENENTECH INC.
 PA Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 PI Wu TD;
 XX WPI: 2004-419628/39.
 DR N-PSDB; ADP23387.
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX Claim 7; SEQ ID NO 566; 2940pp; English.
 XX The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoiatic, antiallergic,
 CC antiaschmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR WPI; 1998-497862/43.

XX New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent

PT and treat e.g. inflammation, arthritis, septicemia, autoimmune diseases,

PT infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury,

PT AIDS and bone diseases.

XX Disclosure; Page 17-18; 22pp; English.

PS This is the amino acid sequence of human TL2 (also known as TRAIL), which

XX has newly been discovered to be a ligand of human tumour necrosis related

CC receptor TR5 (see AAW76331). This TR5 polypeptide of the invention and

CC TL2 can be used in screening processes for compounds which bind the

CC receptor, or its ligand, and which activate (agonists) or inhibit

CC (antagonists) the receptor or TL2. Treatment of a subject with the need

CC to inhibit TR5 polypeptide activity comprises administering an antagonist

CC to the polypeptide, administering a nucleic acid that inhibits the

CC expression of the nucleotide sequence encoding the polypeptide and/or

CC administering a polypeptide that competes with the polypeptide for its

CC ligand, substrate or receptor. The active agents can be used for the

CC treatment of chronic and acute inflammation, arthritis, septicemia,

CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),

CC transplant rejection, graft vs host disease, infection, stroke,

CC ischaemia, acute respiratory disease syndrome, restenosis, brain injury,

CC AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders),

CC atherosclerosis and Alzheimer's disease

XX Sequence 279 AA;

Query Match 99.3%; Score 279; DB 2; Length 279;

Best Local Similarity 100.0%; Pred. No. 2.6e-264;

Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVGGPSLGTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKEDD 62

DB 1 MMEVGGPSLGTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKEDD 60

QY 63 SYWDNDEESMNSPCWQVQWQLRQLVRKMLRTSETISTVQEKQNIISPLVRERGPQRV 122

DB 61 SYWDNDEESMNSPCWQVQWQLRQLVRKMLRTSETISTVQEKQNIISPLVRERGPQRV 120

QY 123 AAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVIEHKGFY 182

DB 121 AAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVIEHKGFY 180

QY 183 YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLYSI 242

DB 181 YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLYSI 240

QY 243 YGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

DB 241 YGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 279

RESULT 58

AAW95032

ID AAW95032 standard; protein; 279 AA.

XX AAW95032;

AC AAW95032;

XX Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.

DT 13-MAY-1999 (first entry)

XX Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;

XX inflammation; septicemia; autoimmune disease; transplant rejection;

KW graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;

KW acute respiratory disease syndrome; restenosis; bone disease; cancer;

KW atherosclerosis; Alzheimer's disease.

OS Unidentified.

XX EP897114-A2.

XX 17-FEB-1999.

XX 04-JUN-1998; 98EP-00304424.

XX 13-AUG-1997; 97US-0055513P.

PR 26-AUG-1997; 97US-0056980P.

PR 29-AUG-1997; 97US-0057550P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA Bringham-Burke MR, Young PR;

XX WPI; 1999-134308/12.

XX Identifying agonists and antagonists to tumour necrosis factor receptor

PT (TNF-R) related polypeptides (LR1, LR2, LR2 and LR4) - useful for

PT treating stroke, Alzheimer's disease and AIDS.

XX Disclosure; Page 14-15; 18pp; English.

XX The invention relates to identifying agonists or antagonists to tumour

CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2

CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a

CC candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2

CC or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)

CC assessing the ability of the candidate compound to compete with TR1 or

CC TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful

CC for treating diseases caused by imbalance of TL or TR polypeptide levels,

CC which cause: chronic and acute inflammation, arthritis, septicemia,

CC autoimmune diseases, transplant rejection, graft vs. host disease,

CC infection, stroke, ischemia, acute respiratory disease syndrome,

CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and

CC Alzheimer's disease. The present sequence represents a TNF-R related

CC polypeptide TL2

XX Sequence 279 AA;

Query Match 99.3%; Score 279; DB 2; Length 279;

Best Local Similarity 100.0%; Pred. No. 2.6e-264;

Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVGGPSLGTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKEDD 62

DB 1 MMEVGGPSLGTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKEDD 60

QY 63 SYWDNDEESMNSPCWQVQWQLRQLVRKMLRTSETISTVQEKQNIISPLVRERGPQRV 122

DB 61 SYWDNDEESMNSPCWQVQWQLRQLVRKMLRTSETISTVQEKQNIISPLVRERGPQRV 120

QY 123 AAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVIEHKGFY 182

DB 121 AAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVIEHKGFY 180

QY 183 YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLYSI 242

DB 181 YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLYSI 240

QY 243 YGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

DB 241 YGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 279

RESULT 59

AAV27018

ID AAV27018 standard; protein; 281 AA.

XX AAV27018;

AC AAV27018;

XX 24-SEP-1999 (first entry)

DE Human Apo-2 ligand (Apo-2L) variant D269A.

XX

Query Match 93.6%; Score 263; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-249;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYNDPDESMNSPCWQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
 DB 61 DDSYNDPDESMNSPCWQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120

QY 121 RVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSNCSKDAEYGLY 240
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNE 263
 DB 241 SIYQGGIFELKENDRIFVSVTNE 263

RESULT 61
 ADB61494
 ID ADB61494 standard; protein; 281 AA.
 AC ADB61494;
 XX
 DT 04-DEC-2003 (first entry)
 DE Human Apo-2 ligand protein mutant E263C.
 KW Apo-2 ligand; DR5-Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX
 OS Synthetic.
 OS Homo sapiens.
 FH Key
 FT Location/Qualifiers
 FT Misc-difference 263 /note= "Native residue of Glu is substituted by Cys"
 FT
 XX WO2003029420-A2.
 PN 10-APR-2003.
 XX
 XX 01-OCT-2002; 2002WO-US031210.
 XX
 XX 02-OCT-2001; 2001US-0326622P.
 PR
 XX (GETH) GENENTECH INC.
 XX
 XX Kelley RF, Lindstrom SH;
 PI
 XX WPI; 2003-541400/51.
 DR
 XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
 PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.
 XX
 XX Claim 1; Page; 92pp; English.
 PS
 XX The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at

CC residue positions identified from x-ray crystal structure of the
 CC DR5-Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, R134C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, K179C, D234C, R249C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5-Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5-Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant E263C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.

XX Sequence 281 AA;

Query Match 93.2%; Score 262; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.1e-247;
 Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYNDPDESMNSPCWQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
 DB 61 DDSYNDPDESMNSPCWQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120

QY 121 RVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSNCSKDAEYGLY 240
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTN 262
 DB 241 SIYQGGIFELKENDRIFVSVTN 262

RESULT 62

ADB61493
 ID ADB61493 standard; protein; 281 AA.

XX
 AC ADB61493;

XX
 DT 04-DEC-2003 (first entry)

XX
 DE Human Apo-2 ligand protein mutant R255C.

XX Apo-2 ligand; DR5-Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.

XX Synthetic.

OS Homo sapiens.

XX
 FH Key Location/Qualifiers

FT Misc-difference 255 /note= "Native residue of Arg is substituted by Cys"
XX WO2003029420-A2.
XX 10-APR-2003.
XX
XX
XX 01-OCT-2002; 2002WO-US031210.
XX 02-OCT-2001; 2001US-0326622P.
XX (GETH) GENENTECH INC.
XX Kelley RF, Lindstrom SH;
XX WPI; 2003-541400/51.
XX
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
XX cancer or an immune-related disease such as multiple sclerosis, comprises
XX amino acid substitutions in the native sequence of the Apo-2 ligand.
XX
XX Claim 1; Page; 92pp; English.
XX
XX The invention relates to a novel isolated Apo-2 ligand variant
XX polypeptide having a sequence that differs from the native sequence
XX having 281 amino acids given in specification. The Apo-2 ligand variant
XX polypeptide is selected from a polypeptide having substitutions at
XX residue positions identified from x-ray crystal structure of the
XX DR5.Apo2L complex. The polypeptide having the substitutions made at
XX residue position(s) selected from 20 positions such as S96C, S101C,
XX S111C, V114C, R115C, E116C, N134C, E144C, N152C, S153C, R170C,
XX R170K, K170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
XX residue position is, outside of the receptor contact region of the
XX DR5.Apo2L complex, and displays high solvent accessibility in the crystal
XX structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
XX and further compositions have the following activities: cytostatic,
XX antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
XX an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
XX inducing apoptosis in mammalian cells, by exposing mammalian cells
XX expressing a receptor selected from DR4 receptor and DR5 receptor to a
XX therapeutically effective amount of the Apo-2 ligand variant polypeptide,
XX colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
XX the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
XX treating cancer (such as lung, breast, colon or colorectal cancer) or an
XX immune-related disease (such as arthritis or multiple sclerosis) in a
XX mammal, by administering to the mammal an effective amount of the Apo-2
XX ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
XX trimer. This sequence represents the human Apo-2 ligand mutant R255C
XX protein of the invention. NOTE: This sequence is not shown in the
XX specification. It has been created from information provided in claim 1
XX and from the sequence in Fig 1 of the specification.
XX
XX Sequence 281 AA;
XX
XX Query Match 90.4%; Score 254; DB 7; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-240;
XX Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYFTNELKQMDKYKSGIACFLKE 60
XX |||||
XX 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYFTNELKQMDKYKSGIACFLKE 60
XX |||||
XX 61 DSDYWDNDDESMNSPCWQVKQLVRKMLTSEETISTVQSKQNSPLVRRGPQ 120
XX |||||
XX 61 DSDYWDNDDESMNSPCWQVKQLVRKMLTSEETISTVQSKQNSPLVRRGPQ 120
XX |||||
XX 121 RVAAHITGRGNTLSSPNSKNEALGRKINSWESSRSGHFLSNLHRLNGELVIHEKG 180
XX |||||
XX 121 RVAAHITGRGNTLSSPNSKNEALGRKINSWESSRSGHFLSNLHRLNGELVIHEKG 180
XX |||||
XX 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
XX |||||

Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
Qy 241 SIYOGGIFELKEND 254
|||
Db 241 SIYOGGIFELKEND 254
|||
RESULT 63
ADB61492
ID ADB61492 standard; protein; 281 AA.
XX
XX ADB61492;
XX
XX 04-DEC-2003 (first entry)
XX Human Apo-2 ligand protein mutant E249C.
XX
XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
XX high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
XX trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
XX lung; breast; immune-related disease; arthritis; multiple sclerosis;
XX human; mutant; mutein.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 249 /note= "Native residue of Glu is substituted by Cys"
XX
XX WO2003029420-A2.
XX
XX 10-APR-2003.
XX
XX 01-OCT-2002; 2002WO-US031210.
XX
XX 02-OCT-2001; 2001US-0326622P.
XX (GETH) GENENTECH INC.
XX
XX Kelley RF, Lindstrom SH;
XX WPI; 2003-541400/51.
XX
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
XX cancer or an immune-related disease such as multiple sclerosis, comprises
XX amino acid substitutions in the native sequence of the Apo-2 ligand.
XX
XX Claim 1; Page; 92pp; English.
XX
XX The invention relates to a novel isolated Apo-2 ligand variant
XX polypeptide having a sequence that differs from the native sequence
XX having 281 amino acids given in specification. The Apo-2 ligand variant
XX polypeptide is selected from a polypeptide having substitutions at
XX residue positions identified from x-ray crystal structure of the
XX DR5.Apo2L complex. The polypeptide having the substitutions made at
XX residue position(s) selected from 20 positions such as S96C, S101C,
XX S111C, V114C, R115C, E116C, N134C, E144C, N152C, S153C, R170C,
XX R170K, K170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
XX residue position is, outside of the receptor contact region of the
XX DR5.Apo2L complex, and displays high solvent accessibility in the crystal
XX structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
XX and further compositions have the following activities: cytostatic,
XX antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
XX an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
XX inducing apoptosis in mammalian cells, by exposing mammalian cells
XX expressing a receptor selected from DR4 receptor and DR5 receptor to a
XX therapeutically effective amount of the Apo-2 ligand variant polypeptide,
XX colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
XX the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
XX treating cancer (such as lung, breast, colon or colorectal cancer) or an
XX immune-related disease (such as arthritis or multiple sclerosis) in a
XX mammal, by administering to the mammal an effective amount of the Apo-2
XX ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
XX trimer. This sequence represents the human Apo-2 ligand mutant R255C
XX protein of the invention. NOTE: This sequence is not shown in the
XX specification. It has been created from information provided in claim 1
XX and from the sequence in Fig 1 of the specification.
XX
XX Sequence 281 AA;
XX
XX Query Match 90.4%; Score 254; DB 7; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-240;
XX Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYFTNELKQMDKYKSGIACFLKE 60
XX |||||
XX 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYFTNELKQMDKYKSGIACFLKE 60
XX |||||
XX 61 DSDYWDNDDESMNSPCWQVKQLVRKMLTSEETISTVQSKQNSPLVRRGPQ 120
XX |||||
XX 61 DSDYWDNDDESMNSPCWQVKQLVRKMLTSEETISTVQSKQNSPLVRRGPQ 120
XX |||||
XX 121 RVAAHITGRGNTLSSPNSKNEALGRKINSWESSRSGHFLSNLHRLNGELVIHEKG 180
XX |||||
XX 121 RVAAHITGRGNTLSSPNSKNEALGRKINSWESSRSGHFLSNLHRLNGELVIHEKG 180
XX |||||
XX 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240
XX |||||

CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant E249C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.
 XX
 SQ Sequence 281 AA;

Query Match 88.3%; Score 248; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 5.6e-234;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DSYWDPNDEESMNSPCQVKQWLRLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DSYWDPNDEESMNSPCQVKQWLRLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
 DB 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
 QY 241 SIYQGIF 248
 DB 241 SIYQGIF 248

RESULT 64
 AA01516
 ID AA01516 standard; peptide; 281 AA.
 AC AA01516;
 XX
 DT 27-MAY-1999 (first entry)
 DE Protein associated with neurodegenerative and autoimmune diseases.
 XX
 KW Neurodegenerative disease; autoimmune disease; inflammatory disease;
 KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
 KW surface receptor; TRAIL protein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 245 /note= "Gly or Cys"
 FT
 XX
 PN FR2766713-A1.
 PD
 XX
 PF 05-FEB-1999.
 XX
 PF 04-AUG-1997; 97FR-00010176.
 PR 04-AUG-1997; 97FR-00010176.
 XX
 PA (INMR) BIO MERIEUX.
 PI Rieger F, Belliveau JF, Perron H;
 XX
 DR WPI; 1999-156177/14.
 XX
 PT Use of polypeptide derived from TRAIL protein for diagnosis of
 PT degenerative disease - autoimmunity and inflammation, also useful in
 PT prevention or treatment, and similar use of corresponding ligand and
 PT nucleic acid.
 XX

PS Claim 1; Page 13; 21pp; French.

CC The specification describes the use a polypeptide corresponding to at
 CC least the primary sequence of part of the present sequence to produce a
 CC diagnostic, prophylactic or therapeutic composition useful in cases of
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
 CC be used in treatment of neurodegenerative diseases, lupus erythematosus,
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
 CC nervous system cells, antigenic and specifically recognise the surface
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
 CC receptors, inhibiting formation of natural complex
 XX
 SQ Sequence 281 AA;

Query Match 86.8%; Score 244; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 4.6e-230;
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DSYWDPNDEESMNSPCQVKQWLRLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DSYWDPNDEESMNSPCQVKQWLRLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
 DB 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
 QY 241 SIYQ 244
 DB 241 SIYQ 244

RESULT 65
 AA72935
 ID AA72935 standard; protein; 266 AA.
 AC AA72935;
 XX
 DT 11-SEP-2003 (revised)
 DT 13-JUN-2001 (first entry)
 XX
 DE OmpA signal peptide-human TRAIL fusion protein.
 XX
 KW Human; attenuated tumour-targeted bacteria; effector molecule;
 KW tumour necrosis factor; TNF; anti-angiogenic factor;
 KW cytotoxic polypeptide; tumour inhibitory enzyme; therapy; carcinoma;
 KW melanoma; lymphoma; sarcoma; metastasis; cyostatic; fusion protein;
 KW TNF-alpha-related apoptosis-inducing ligand; TRAIL.
 XX
 OS Homo sapiens.
 OS Escherichia coli.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21 /label= OmpA_signal_peptide
 FT Region 23..266 /note= "Mature human TNF-alpha-related apoptosis-inducing
 FT ligand"
 XX
 PN WO200125397-A2.
 XX
 PD 12-APR-2001.
 XX

PF 24-AUG-2000; 2000WO-US0323242.
XX
PR 04-OCT-1999; 99US-0157500P.
PR 04-OCT-1999; 99US-0157581P.
PR 04-OCT-1999; 99US-0157637P.
XX
PA (VION-) VION PHARM INC.
XX
XX Bermudes DG, King IC, Clairmont CA, Lin SL, Belcourt M;
PI
XX WPI; 2001-245063/25.
DR N-PSDB; AAD03112.
XX
PT Attenuated tumor-targeted bacteria comprising nucleic acids encoding
PT primary and secondary effector molecules, useful for the treatment of
PT e.g. carcinomas, melanomas, lymphomas and sarcomas.
XX
PS Example 7; Fig 6; 185pp; English.
XX
CC The present invention relates to the preparation and use of attenuated
CC tumor-targeted bacteria, such as, e.g., Salmonella, as a vector for the
CC delivery of one or more primary effector molecules and secondary effector
CC molecules to the site of a solid tumour. The primary effector molecules
CC of the invention include members of the tumour necrosis factor (TNF),
CC anti-angiogenic factors, cytotoxic polypeptides and tumour inhibitory
CC enzymes. They induce a local immune response at the site of the tumour
CC that results in the inhibition of growth of a tumour or tumour cells. The
CC primary effector molecules are used for the treatment of solid tumours
CC such as carcinomas, melanomas, lymphomas, sarcomas or metastases derived
CC from these tumours. The present sequence is OmpA signal peptide-mature
CC human TNF-alpha-related apoptosis-inducing ligand (TRAIL) fusion protein.
CC The fusion of OmpA signal peptide to the amino terminus of TRAIL effector
CC molecule enhances the periplasmic localisation and subsequent processing
CC of the effector molecule. (Updated on 11-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 266 AA;

Query Match 86.1%; Score 242; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 4e-228;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 NELKQMDKYSGKGIACFLKEDDSYDNDPEESMNSPCWQVKQLRQLVRKMLRTSEET 99
DB 25 NELKQMDKYSGKGIACFLKEDDSYDNDPEESMNSPCWQVKQLRQLVRKMLRTSEET 84

QY 100 ISTVQEKQNI SPLVRERGPQVAHITGTRGRSNTLSPPNSKNKALGRKINSWESSRS 159
DB 85 ISTVQEKQNI SPLVRERGPQVAHITGTRGRSNTLSPPNSKNKALGRKINSWESSRS 144

QY 160 GHSFLSNLHRLNGELVIEHKGFIYYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPP 219
DB 145 GHSFLSNLHRLNGELVIEHKGFIYYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPP 204

QY 220 ILLMKSARNSCWSKDAEYGLYSIQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAPL 279
DB 205 ILLMKSARNSCWSKDAEYGLYSIQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAPL 264

QY 280 VG 281
DB 265 VG 266

RESULT 66
ADB61491
ID ADB61491 standard; protein; 281 AA.
XX
AC ADB61491;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human Apo-2 ligand protein mutant D234C.
XX

KW Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW human; mutant; mutein.
XX
OS Synthetic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 234 /note= "Native residue of Asp is substituted by Cys"
FT WO2003029420-A2.
XX
PD 10-APR-2003.
XX
PF 01-OCT-2002; 2002WO-US031210.
XX
PR 02-OCT-2001; 2001US-0326622P.
XX (GETH) GENENTECH INC.
XX Kelley RF, Lindstrom SH;
XX WPI; 2003-541400/51.
XX
Novel isolated Apo-2 ligand variant polypeptide useful for treating
cancer or an immune-related disease such as multiple sclerosis, comprises
amino acid substitutions in the native sequence of the Apo-2 ligand.

Claim 1; Page; 92pp; English.

The invention relates to a novel isolated Apo-2 ligand variant
polypeptide having a sequence that differs from the native sequence
having 281 amino acids given in specification. The Apo-2 ligand variant
polypeptide is selected from a polypeptide having substitutions at
residue positions identified from x-ray crystal structures of the
DR5.Apo2L complex. The polypeptide having the substitutions made at
residue position(s) selected from 20 positions such as S96C, S101C,
S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
R170K, R170S, K179C, E234C, E249C, R255C, E263C, H264C, such that the
residue position is, outside of the receptor contact region of the
DR5.Apo2L complex, and displays high solvent accessibility in the crystal
structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
and further compositions have the following activities: cytostatic,
antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
inducing apoptosis in mammalian cells, by exposing mammalian cells
expressing a receptor selected from DR4 receptor and DR5 receptor to a
therapeutically effective amount of the Apo-2 ligand variant polypeptide,
Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
treating cancer (such as lung, breast, colon or colorectal cancer) or an
immune-related disease (such as arthritis or multiple sclerosis) in a
mammal, by administering to the mammal an effective amount of the Apo-2
ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
trimer. This sequence represents the human Apo-2 ligand mutant D234C
protein of the invention. NOTE: This sequence is not shown in the
specification. It has been created from information provided in claim 1
and from the sequence in Fig 1 of the specification.

Sequence 281 AA;

Query Match 82.9%; Score 233; DB 7; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.7e-219;

Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGGTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVQGGPSLGGTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

QY 61 DSYNDPNDDESMNSPCQVKQKQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 DB 61 DSYNDPNDDESMNSPCQVKQKQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180
 QY 181 FYYIISQTYFRQEBEIKENTKDKQKQVQIYKYTSYPPDPILLMKSARNCSWSK 233
 DB 181 FYYIISQTYFRQEBEIKENTKDKQKQVQIYKYTSYPPDPILLMKSARNCSWSK 233

RESULT 67
 AAY27017
 ID AAY27017 standard; protein; 281 AA.
 XX
 AC AAY27017;
 XX
 DT 24-SEP-1999 (first entry)
 DE Human Apo-2 ligand (Apo-2L) variant D218A.
 KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
 KW lupus; immune-mediated glomerular nephritis; human; variant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 218 /label= D218A
 FT /note= "wild-type Asp is replaced with Ala"
 XX
 XX WO9936535-A1.
 XX
 XX 22-JUL-1999.
 PD
 XX
 PF 15-JAN-1999; 99WO-US001039.
 XX
 PR 15-JAN-1998; 98US-00007886.
 PR 15-APR-1998; 98US-00060533.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;
 PI WPI; 1999-444397/37.
 DR
 XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 FT in mammalian cancer cells.
 FT
 XX Claim 10; Page; 86pp; English.
 PS
 XX The invention relates to a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis. Sequences AAY27016-19 represent
 CC specific examples of Apo-2L variants. Note: This sequence is not provided
 CC in the specification. It has been created by modifying the wild-type Apo-
 CC 2L sequence provided in Fig 1A

Sequence 281 AA;
 SQ

Query Match 77.2%; Score 217; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.2e-203;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60
 QY 61 DSYNDPNDDESMNSPCQVKQKQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 DB 61 DSYNDPNDDESMNSPCQVKQKQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHEKG 180
 QY 181 FYYIISQTYFRQEBEIKENTKDKQKQVQIYKYTSYP 217
 DB 181 FYYIISQTYFRQEBEIKENTKDKQKQVQIYKYTSYP 217

RESULT 68
 AAY27019
 ID AAY27019 standard; protein; 281 AA.
 XX
 AC AAY27019;
 XX
 DT 24-SEP-1999 (first entry)
 DE Human Apo-2 ligand (Apo-2L) variant D203A, D218A, D269A.
 KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
 KW lupus; immune-mediated glomerular nephritis; human; variant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 203 /label= D203A
 FT /note= "wild-type Asp is replaced with Ala"
 FT Misc-difference 218 /label= D218A
 FT /note= "wild-type Asp is replaced with Ala"
 FT Misc-difference 269 /label= D269A
 FT /note= "wild-type Asp is replaced with Ala"
 XX
 XX WO9936535-A1.
 PN
 XX
 XX 22-JUL-1999.
 PD
 XX
 PF 15-JAN-1999; 99WO-US001039.
 XX
 PR 15-JAN-1998; 98US-00007886.
 PR 15-APR-1998; 98US-00060533.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;
 PI WPI; 1999-444397/37.
 DR
 XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 FT in mammalian cancer cells.
 FT
 XX Claim 12; Page; 86pp; English.
 PS
 XX The invention relates to a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic

CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
CC associated with increased apoptosis. Sequences AAY27016-19 represent
CC specific examples of Apo-2L variants. Note: This sequence is not provided
CC in the specification. It has been created by modifying the wild-type Apo-
CC 2L sequence provided in Fig 1A

XX
SQ Sequence 281 AA;
Query Match 71.9%; Score 202; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.8e-189; Indels 0; Gaps 0;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVKQWLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCQVKQWLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKN 202
Db 181 FYIYSQTYFRFQEEIKENTKN 202

RESULT 69
AAY27016
ID AAY27016 standard; protein; 281 AA.
AC AAY27016;
XX
DT 24-SEP-1999 (first entry)
XX
DE Human Apo-2 ligand (Apo-2L) variant D203A.
XX
KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
KW lupus; immune-mediated glomerular nephritis; human; variant.
XX
OS Homo sapiens.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Misc-difference 203 /label= D203A
FT /note= "wild-type Asp is replaced with Ala"
XX
PN WO936535-A1.
XX
PD 22-JUL-1999.
XX
PF 15-JAN-1999; 99WO-US001039.
XX
PR 15-JAN-1998; 98US-00007886.
PR 15-APR-1998; 98US-00060533.
XX
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;
XX WPI; 1999-444397/37.
XX
XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
XX in mammalian cancer cells.
XX
XX Claim 9; Page; 86pp; English.

XX
CC The invention relates to a novel human cytokine, designated Apo-2 ligand
CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer

CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
CC induce apoptosis for pathological conditions characterized by decreased
CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
CC coding sequence can also be used in quantitative and screening diagnostic
CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
CC associated with increased apoptosis. Sequences AAY27016-19 represent
CC specific examples of Apo-2L variants. Note: This sequence is not provided
CC in the specification. It has been created by modifying the wild-type Apo-
CC 2L sequence provided in Fig 1A

XX
SQ Sequence 281 AA;
Query Match 71.9%; Score 202; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.8e-189; Indels 0; Gaps 0;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVKQWLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCQVKQWLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKN 202
Db 181 FYIYSQTYFRFQEEIKENTKN 202

RESULT 70
ABG72257
ID ABG72257 standard; protein; 281 AA.
XX
AC ABG72257;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human tumour related apoptosis inducing ligand (Trail).
XX
KW Human; tumour related apoptosis inducing ligand; Trail;
KW Trail; prokaryotic expression system; tumour cell death.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 217 /note= "Encoded by CTT"
FT
XX
PN CN1354183-A.
XX
PD 19-JUN-2002.
XX
PF 30-NOV-2001; 2001CN-00132371.
XX
PR 30-NOV-2001; 2001CN-00132371.
XX
PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
XX
XX Hu Y, Yao Y;
XX WPI; 2002-751439/82.
XX N-PSDB; ABX14391.
XX
XX Tumor death induction ligand gene, gene expression protein and its
XX preparation method.
XX
XX Claim 7; Page 10 (disclosure); 17pp; Chinese.

CC The present invention relates to the isolation of cDNA encoding human
 CC tumour related apoptosis inducing ligand (TRAIL), and the TRAIL protein.
 CC The TRAIL full length cDNA is cloned, and is utilised to create a TRAIL
 CC prokaryotic expression system. The full length TRAIL cDNA is used to
 CC respectively clone cDNA of soluble ectocytic segment Trail109 and Trail
 CC 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic
 CC expression systems. The prokaryotic expression systems created greatly
 CC increase the expression and quantity of the TRAIL, Trail109, and Trail114
 CC proteins, and may be useful in a new preparation for killing tumour
 CC cells. The present sequence represents the full length human TRAIL
 CC protein
 XX
 SQ Sequence 281 AA;

Query Match 70.8%; Score 199; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 5e-186;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYSGKIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYSGKIACFLKE 60
 QY 61 DSDYDNDDEESMNSPCQVKQKQLRQVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
 DB 61 DSDYDNDDEESMNSPCQVKQKQLRQVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180
 QY 181 FYIYISQTYFRFQEEIKEN 199
 DB 181 FYIYISQTYFRFQEEIKEN 199

RESULT 71

AAU99301 ID AAU99301 standard; protein; 212 AA.

XX AC AAU99301;
 XX
 DT 24-SEP-2002 (first entry)
 XX Human TRAIL splice variant 8, rpl-6-6, protein.
 KW Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
 KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
 KW TRAIL; apoptosis; programmed cell death; differentiation; development;
 KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
 KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
 KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
 KW chromosome 3q26; rpl-6-6.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 1..16
 FT /note= "Cytoplasmic domain"
 FT Domain 17..38
 FT /note= "Transmembrane domain"
 FT Domain 39..212
 FT /note= "Extracellular domain"
 FT Misc-difference 209
 FT /note= "Encoded by in-frame stop codon"

XX US2002061525-A1.

XX 23-MAY-2002.

XX 16-MAY-2001; 2001US-00855544.

XX 16-MAY-2000; 2000IL-00136156.

XX

PA (YELI/) YELIN R.
 PA (KHOS/) KHOSRAVI R.
 PA (SAVI/) SAVITZKY R.

PI Yelin R, Khosravi R, Savitzky K;

XX WPI; 2002-479259/51.

DR
 XX New splice variants of tumor necrosis factor-related apoptosis inducing
 PT ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat
 PT diseases or disorders associated with low expression of the variants.

XX Claim 4; Fig 8; 29pp; English.

XX The invention discloses isolated, naturally occurring, polypeptide splice
 CC variants of human tumour necrosis factor (TNF)-related apoptosis inducing
 CC ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal
 CC cellular differentiation and development of multicellular organisms.
 CC Apoptosis is induced by certain cytokines which include TNF and TRAIL
 CC (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane
 CC protein which induces apoptosis and nuclear factor-B (NF-B) activation in
 CC many tissues and cells. Receptors for TRAIL include two death domain
 CC containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1
 CC and DcR2, lacking the intracellular signalling death domain. TRAIL,
 CC induced by type I interferons, induces apoptosis in tumour cells, whereas
 CC normal cells are relatively resistant without showing significant toxic
 CC side effects. Thus, TRAIL has the potential to be a very useful
 CC antitumour agent. The naturally occurring splice variants may differ in
 CC their cellular distribution, expression levels/timing and activity.
 CC Determining these factors could provide possible mechanisms for the
 CC induction of apoptosis of tumours cells. The splice variant polypeptides
 CC and polynucleotides can be used in gene therapy, to raise antibodies, to
 CC detect the levels, distribution and ratios of expression of TRAIL, and
 CC its splice variants, in a biological sample and to identify compounds
 CC which bind the variant TRAIL products and modulate its activity (agonists
 CC and antagonists). Pharmaceutical compositions, comprising an expression
 CC vector or any of the amino acid sequences, are useful for causing a
 CC cytotoxic effect in cancer cells and for treatment of diseases which can
 CC be ameliorated, cured or prevented by lowering or raising the level of
 CC the amino acid sequences. The antibodies may also have a therapeutic
 CC utility in blocking or decreasing the activity of the TRAIL variant
 CC products. Diseases that may be treated include cancer, neurodegenerative
 CC diseases, autoimmune diseases, diseases involved in the non-normal
 CC development of tissues and aging. TRAIL's gene is located on chromosome
 CC 3q26. The sequence presented is the human TNF-related apoptosis inducing
 CC ligand (TRAIL) splice variant 8, rpl-6-6, protein which has had an C-
 CC terminal section of the conserved TNF domain deleted

XX Sequence 212 AA;

Query Match 68.7%; Score 193; DB 5; Length 212;
 Best Local Similarity 100.0%; Pred. No. 3e-180;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYSGKIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYSGKIACFLKE 60
 QY 61 DSDYDNDDEESMNSPCQVKQKQLRQVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
 DB 61 DSDYDNDDEESMNSPCQVKQKQLRQVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKG 180
 QY 181 FYIYISQTYFRFQ 193
 DB 181 FYIYISQTYFRFQ 193

RESULT 72
 ADK72306

Query Match 66.9%; Score 188; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-175;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120
DB 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYISQT 188
DB 181 FYIYISQT 188

RESULT 74
ADK72305
ID ADK72305 standard; protein; 281 AA.
XX AC ADK72305;
XX DT 06-MAY-2004 (first entry)
XX DE Human Apo-2 ligand variant #1.
XX KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;
XX KW variant; cancer; immune system disease; arthritis; multiple sclerosis;
XX KW human; mutein.
XX OS Homo sapiens.
XX OS Synthetic.

Key Location/Qualifiers
FT Misc-difference 189 /note= "wild-type Tyr replaced by Ala"
FT Misc-difference 191 /note= "wild-type Arg replaced by Lys"
FT Misc-difference 193 /note= "wild-type Gln replaced by Lys"
XX PN WO2004001009-A2.
XX PD 31-DEC-2003.
XX PF 23-JUN-2003; 2003WO-US019750.
XX PR 24-JUN-2002; 2002US-0391050P.
XX PA (GETH) GENENTECH INC.
XX PI Hymowitz S, Kelley RF, Lindstrom SH;
XX DR WPI; 2004-082490/08.
XX FT New Apo-2 ligand variant polypeptide, useful for preparing a composition
XX FT for treating cancer or immune-related disease, e.g., arthritis or
XX FT multiple sclerosis.
XX PS Claim 9; Page; 11pp; English.

The invention relates to a novel isolated Apo-2 ligand variant polypeptide, comprising a sequence that differs from the native sequence Apo-2 ligand polypeptide sequence comprising 282 amino acids and having one or more following amino acid substitutions at the residue positions comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand

CC variant polypeptide. Further disclosed are a composition comprising the Apo-2 ligand variant polypeptide, a method of treating cancer, and a method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant polypeptide is useful for preparing a composition for treating cancer or immune-related disease, e.g., arthritis or multiple sclerosis. The current sequence represents a human Apo-2 ligand mutant. Note: This sequence is not found in the specification, but may be created using the wild-type Apo-2 ligand sequence given in ADK72296.

XX SQ Sequence 281 AA;

Query Match 66.9%; Score 188; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-175;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120
DB 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPG 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYISQT 188
DB 181 FYIYISQT 188

RESULT 75
ADK72309
ID ADK72309 standard; protein; 281 AA.
XX AC ADK72309;
XX DT 06-MAY-2004 (first entry)
XX DE Human Apo-2 ligand variant #5.
XX KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;
XX KW variant; cancer; immune system disease; arthritis; multiple sclerosis;
XX KW human; mutein.
XX OS Homo sapiens.
XX OS Synthetic.

Key Location/Qualifiers
FT Misc-difference 189 /note= "wild-type Tyr replaced by Ala"
FT Misc-difference 191 /note= "wild-type Arg replaced by Lys"
FT Misc-difference 193 /note= "wild-type Gln replaced by Arg"
FT Misc-difference 264 /note= "wild-type His replaced by Ser"
FT Misc-difference 266 /note= "wild-type Ile replaced by Leu"
FT Misc-difference 269 /note= "wild-type Asp replaced by Glu"
XX PN WO2004001009-A2.
XX PD 31-DEC-2003.
XX PF 23-JUN-2003; 2003WO-US019750.
XX PR 24-JUN-2002; 2002US-0391050P.
XX PA (GETH) GENENTECH INC.
XX XX

PI Hymowitz S, Kelley RF, Lindstrom SH;
XX
DR WPI; 2004-082490/08.
XX
PT New Apo-2 ligand variant polypeptide, useful for preparing a composition
PT for treating cancer or immune-related disease, e.g., arthritis or
XX multiple sclerosis.
XX
PS Claim 9; Page; 111pp; English.
XX
CC The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide, comprising a sequence that differs from the native sequence
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having
CC one or more following amino acid substitutions at the residue positions
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
CC variant polypeptide. Further disclosed are a composition comprising the
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant
CC polypeptide is useful for preparing a composition for treating cancer or
CC immune-related disease, e.g., arthritis or multiple sclerosis. The
CC current sequence represents a human Apo-2 ligand mutant. Note: This
CC sequence is not found in the specification, but may be created using the
CC wild-type Apo-2 ligand sequence given in ADK72296.
XX
SQ Sequence 281 AA;

Query Match 66.9%; Score 188; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-175;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKOMODKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKOMQDKYKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

QY 121 RVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
DB 121 RVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180

QY 181 FYIYSQT 188
DB 181 FYIYSQT 188

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:52:03 ; Search time 161 Seconds
(without alignments)
670.176 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHESFFGAFLVG 281

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1714042 seqs, 383979560 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	281	100.0	281	8	US-08-916-6259-6
2	281	100.0	281	8	US-08-971-317A-8
3	281	100.0	281	9	US-09-813-329-17
4	281	100.0	281	9	US-09-193-663-8
5	281	100.0	281	9	US-09-934-465-1
6	281	100.0	281	10	US-09-919-039-118
7	281	100.0	281	13	US-10-011-125-4
8	281	100.0	281	13	US-10-001-054-54
9	281	100.0	281	14	US-10-093-766-54
10	281	100.0	281	14	US-10-174-654-11
11	281	100.0	281	14	US-10-151-882-41
12	281	100.0	281	14	US-10-218-547-20
13	281	100.0	281	14	US-10-322-673-72
14	281	100.0	281	14	US-10-139-785-66
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17	281	100.0	281	15	US-10-292-486-5
18	281	100.0	281	15	US-10-333-712-1
19	281	100.0	281	15	US-10-662-429-2
20	281	100.0	281	15	US-10-202-062-20
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25	281	100.0	281	16	US-10-755-889-210
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32	281	100.0	281	16	US-10-861-685-1
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36	281	100.0	281	17	US-10-495-353-1
37	281	100.0	281	17	US-10-652-979-1
38	279	99.3	279	13	US-10-066-209-3
39	242	86.1	266	16	US-10-367-094-22
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46	187	66.5	480	15	US-10-389-223A-4
47	187	66.5	614	15	US-10-389-223A-2
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49	168	59.8	168	17	US-10-981-989-14
50	168	59.8	228	17	US-10-855-559-4
51	168	59.8	365	16	US-10-723-003-64
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53	166	59.1	166	9	US-09-779-050A-16
54	161	57.3	161	14	US-10-216-074-7
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56	161	57.3	161	16	US-10-611-399-11
57	161	57.3	161	17	US-10-794-751-11
58	158	56.2	158	17	US-10-778-890-10
59	156	55.5	296	14	US-10-185-425-5
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61	141	50.2	169	16	US-10-781-866-29
62	141	50.2	246	9	US-09-855-544A-13
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64	130	46.3	283	17	US-10-978-203-23
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66	127	45.2	164	13	US-10-116-378-29
67	127	45.2	164	17	US-10-959-537-29
68	117	41.6	270	17	US-10-006-305A-8
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71	90	32.0	98	9	US-09-855-544A-10
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78	85	30.2	85	16	US-10-890-368-12
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80	56	19.9	56	15	US-10-399-018-20
81	44	15.7	50	9	US-09-864-761-33427
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Sequence 18, Appl
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85 34 12.1 34 14 US-10-272-411-24
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87 15 5.3 15 17 US-10-625-073-14
88 15 5.3 19 17 US-10-625-073-32
89 14 5.0 172 9 US-09-773-050A-17
90 14 5.0 287 16 US-10-367-094-15
91 14 5.0 291 10 US-09-873-829-6
92 14 5.0 291 13 US-10-017-910-6
93 14 5.0 291 15 US-10-652-244-6
94 12 4.3 87 14 US-10-286-696-13
95 12 4.3 87 16 US-10-890-368-13
96 12 4.3 87 16 US-10-889-948-13
97 11 3.9 21 15 US-10-399-018-21
98 10 3.6 10 14 US-10-272-411-25
99 10 3.6 10 14 US-10-272-328A-25
100 9 3.2 9 14 US-10-272-411-27

ALIGNMENTS

RESULT 1
US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Publication No. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; TITLE OF INVENTION: RECEPTOR, TR6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50008-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-916-625B-6

Query Match 100.0%; Score 281; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNKLQKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNKLQKQMDKYKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGPQ 120
Db 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGPQ 120
QY 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAKNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAKNSCWSKDAEYGLY 240
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RESULT 2
US-08-971-317A-8
; Sequence 8, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
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; APPLICATION NUMBER: US/08/971,317A
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mimi C
; REGISTRATION NUMBER: 39,046
; REFERENCE/DOCKET NUMBER: 6255.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010925A1
US-08-971-317A-8

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Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6

US-09-919-039-118
; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118

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Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
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QY 181 FYIYISQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYISQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 7

US-10-011-125-4
; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-011-125-4

Query Match 100.0%; Score 281; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272; Indels 0; Gaps 0;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYISQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWKSDAEYGLY 240
Db 181 FYIYISQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8

US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Shelton, David
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P3034RPCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/096891
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/096894
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100263

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; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/107783
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112420
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/115554
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116533
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/131294
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
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; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/187202
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; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/218517
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/284291
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380913
; PRIOR FILING DATE: 1999-09-09
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; PRIOR FILING DATE: 1999-10-18
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; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/802706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/866034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/882636
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13

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; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US99/00106
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/08615
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28634
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00376
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/06884
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/13705
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/14941
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/22031
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US01/27099

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; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-54

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Query Match	100.0%	Score 281;	DB 13;	Length 281;
Best Local Similarity	100.0%;	Prod. No. 6.4e-272;		
Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAMMEVGGPSLGQTCVLIIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE	60	
Db	1	MAMMEVGGPSLGQTCVLIIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE	60	
Qy	61	DDSYWDDNDESMNSPCWQKWQLRQLVRKMILTSETISTVQEKQONTSPLVREGPQ	120	
Db	61	DDSYWDDNDESMNSPCWQKWQLRQLVRKMILTSETISTVQEKQONTSPLVREGPQ	120	
Qy	121	RVAAHITGTRGRNTLSPNSKNEKALGRKINSWESSRSGSHFSLSNHLRNGELVVIHEKG	180	
Db	121	RVAAHITGTRGRNTLSPNSKNEKALGRKINSWESSRSGSHFSLSNHLRNGELVVIHEKG	180	
Qy	181	FYIYTSQTYFRFQEEIKENTKNDQMVOYIYKYTSPDPILLMKSAENSCWSKDAEYGLY	240	
Db	181	FYIYTSQTYFRFQEEIKENTKNDQMVOYIYKYTSPDPILLMKSAENSCWSKDAEYGLY	240	
Qy	241	SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281	
Db	241	SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281	

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RESULT 9
US-10-093-766-54
; Sequence 54, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Laeek, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpl, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54

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	Query Match	100.0%;	Score 281;	DB 14;	Length 281;
	Best Local Similarity	100.0%;	Prod. No. 6.4e-272;		
	Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVAVYVYFTNELKQWQDKYSKSGIACFLKE	60		
Db	1	MAMMEVGGPSLGGTCTVLIIVFTVLLQSLCAVAVYVYFTNELKQWQDKYSKSGIACFLKE	60		
Qy	61	DDSYDNDNDSESMNSPCQWKVQQLRQLVRXKMLTSTSETSTVQEKQONTSPLVRRGPQ	120		
Db	61	DDSYDNDNDSESMNSPCQWKVQQLRQLVRXKMLTSTSETSTVQEKQONTSPLVRRGPQ	120		
Qy	121	RVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFUSNLHLRNGELVVIHEKG	180		
Db	121	RVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFUSNLHLRNGELVVIHEKG	180		
Qy	181	FYIYISQTYFRFQBEIKENTKNDQMQVQIYKYTYSYDPDIPILLMKASRNSCWSKDAEYGLY	240		

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Db      181 FYIYISQYFRQBEIKENTKNDKQWQYIYKYISYDPDILLMKSGARNCSWSDAEYGLY 240
Qy      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db      241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 10
US-10-174-654-11
; Sequence 11, Application US/10174654
; Publication No. US20030044937A1
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; Mills, Cynthia J
; Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/174,654
; FILING DATE: 19-Jun-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-174-654-11

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	Query Match	100.0%;	Score 281;	DB 14;	Length 281;
	Best Local Similarity	100.0%;	Pred. No. 6.4e-272;		
	Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAMMEVGGPSLGQTCVLIVFTVLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE	60		
Db	1	MAMMEVGGPSLGQTCVLIVFTVLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE	60		
Qy	61	DDSYWDPNDEESMNSPCQWKQRLRLRKMIILRTSEETISTVQEKQOINISPLVRERGQP	120		
Db	61	DDSYWDPNDEESMNSPCQWKQRLRLRKMIILRTSEETISTVQEKQOINISPLVRERGQP	120		
Qy	121	RVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSRSGHSLNLHLRNGELVLIHEKG	180		
Db	121	RVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSRSGHSLNLHLRNGELVLIHEKG	180		
Qy	181	FYIYIGQTYPRFOEIKENTKNDQMQVYIYKTSYSPDPILLMKSRNSCWSKDAEYGLY	240		
Db	181	FYIYISQTYPRFOEIKENTKNDQMQVYIYKTSYSPDPILLMKSRNSCWSKDAEYGLY	240		

Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG	281
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG	281

RESULT 11

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US-10-151-882-41
; Sequence 41, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tu
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-41

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Query Match	100.0%	Score 281;	DB 14;	Length 281;
Best Local Similarity	100.0%;	Pred. No. 6.4e-272;		
Matches ~281; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	MAMMEVGGPSLGTCVLIIIVFTVLLQSCLCAVATTVYVFTNELKQMDKYKSXGIACTFLKE	60	
Db	1	MAMMEVGGPSLGTCVLIIIVFTVLLQSCLCAVATTVYVFTNELKQMDKYKSXGIACTFLKE	60	
Qy	61	DDSYWDNDNDESMNSPCWQVKWQLRQLVRKMILTSETISTVOEKQONISPLVREGRQP	120	
Db	61	DDSYWDNDNDESMNSPCWQVKWQLRQLVRKMILTSETISTVOEKQONISPLVREGRQP	120	
Qy	121	RVAAHITGTGRSNTLSPNSKNEALGRKINSWESSRGHSFSLNLHRLNGELVIIEHG	180	
Db	121	RVAAHITGTGRSNTLSPNSKNEALGRKINSWESSRGHSFSLNLHRLNGELVIIEHG	180	
Qy	181	FYYIYSQTYFRFBQEIKENTKNDAQVQIYKYTSYPDPILLMKSARNCSWKDAEYGLY	240	
Db	181	FYYIYSQTYFRFBQEIKENTKNDAQVQIYKYTSYPDPILLMKSARNCSWKDAEYGLY	240	
Qy	241	SIYOGGIPELKENDRIIFVSVTNEHLIDMDHEASFFGAFLVG	281	
Db	241	SIYOGGIPELKENDRIIFVSVTNEHLIDMDHEASFFGAFLVG	281	

RESULT 12

RA0001 12
 US-10-218-547-20
 ; Sequence 20, Application US/10218547
 ; Publication No. US20030100074A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.
 ; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
 ; TITLE OF INVENTION: Human Endokine Alpha
 ; FILE REFERENCE: PF561
 ; CURRENT APPLICATION NUMBER: US/10/218,547
 ; CURRENT FILING DATE: 2002-08-15
 ; PRIOR APPLICATION NUMBER: 60/312,542
 ; PRIOR FILING DATE: 2001-08-16
 ; PRIOR APPLICATION NUMBER: 60/330,761
 ; PRIOR FILING DATE: 2001-10-30
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 20
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: human
 US-10-218-547-20

[illegible]

RESULT 13
US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PFS85
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-72

	Query Match	100.0%;	Score 281;	DB 14;	Length 281;
	Best Local Similarity	100.0%;	Pred. No. 6.4e-272;		
	Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAMMEVQGGPSLQGT	CVLIVIFTVLLQSLCAVATVYYFTNELQMDKQKSGSGIACFLKE	60	
Db	1	MAMMEVQGGPSLQGT	CVLIVIFTVLLQSLCAVATVYYFTNELQMDKQKSGSGIACFLKE	60	
Qy	61	DSQYDPNDEESNNSPCWVKQRLVRKMLIRTSSEETISTVQEKQKQINISPLVRERGPQ	120		
Db	61	DSQYDPNDEESNNSPCWVKQRLVRKMLIRTSSEETISTVQEKQKQINISPLVRERGPQ	120		
Qy	121	RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHIRNGELVTHKVG	180		
Db	121	RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHIRNGELVTHKVG	180		
Qy	181	FYYIYSQTYFRFQEEIKENTQNDKQWQVQIYKYTSPYDPILLMKSSARNCSWKDAEYGLY	240		

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Db 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSNCSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 14
US-10-139-785-66
; Sequence 66, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-66

Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272; Mismatches 0; Indels 0; Gaps 0;
Matches 281; Conservative 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

Qy 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSNCSKDAEYGLY 240
Db 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSNCSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 15
US-10-310-793-26
; Sequence 26, Application US/10310793
; Publication No. US20030198640A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-310-793-26

Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272; Mismatches 0; Indels 0; Gaps 0;
Matches 281; Conservative 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

Qy 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSNCSKDAEYGLY 240
Db 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSNCSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 16
US-10-279-687-8
; Sequence 8, Application US/10279687
; Publication No. US20030211509A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
```



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; FILE REFERENCE: 6255, US C2
; CURRENT APPLICATION NUMBER: US/10/279,687
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 10/105,738
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/193,663
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/065,916
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-279-687-8

Query Match      100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYYVFTNKLQMDKYSKSGIACFLKE 60
   |||
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYYVFTNKLQMDKYSKSGIACFLKE 60
   |||

QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||
Db 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180
   |||
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180
   |||

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
   |||
Db 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
   |||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
   |||
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
   |||

RESULT 17
US-10-292-486-5
; Sequence 5, Application US/10292486
; Publication No. US20030228309A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies That Immunosepecifically Bind To TRAIL Receptors
; FILE REFERENCE: PF532PI
; CURRENT APPLICATION NUMBER: US/10/292,486
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/403,376
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/377,973
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/331,309
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/986,149
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,359
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/295,018
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/252,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/248,847
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/246,612
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 281
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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-486-5

Query Match      100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYYVFTNKLQMDKYSKSGIACFLKE 60
   |||
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYYVFTNKLQMDKYSKSGIACFLKE 60
   |||

QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||
Db 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180
   |||
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180
   |||

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
   |||
Db 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
   |||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
   |||
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
   |||

RESULT 18
US-10-333-712-1
; Sequence 1, Application US/10333712
; Publication No. US20040005314A1
; GENERAL INFORMATION:
; APPLICANT: Escandon, Enrique
; APPLICANT: Fox, Judith A.
; APPLICANT: Kelley, Sean K.
; APPLICANT: Xiang, Hong
; TITLE OF INVENTION: APO-2L RECEPTOR AGONIST AND CPT-11 SYNERGISM
; FILE REFERENCE: P1838R1
; CURRENT APPLICATION NUMBER: US/10/333,712
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: PCT/US01/23691
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,256
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-333-712-1

Query Match      100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYYVFTNKLQMDKYSKSGIACFLKE 60
   |||
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYYVFTNKLQMDKYSKSGIACFLKE 60
   |||

QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||
Db 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180
   |||
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180
   |||

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
   |||
Db 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
   |||
```

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 19

US-10-662-429-2
; Sequence 2, Application US/10662429
; Publication No. US20040038347A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/662,429
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-429-2

Query Match 100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60
QY 61 DSYWDNDDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQNISPLVVRGPQ 120
Db 61 DSYWDNDDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQNISPLVVRGPQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKTYSPDPILLMKSRNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKTYSPDPILLMKSRNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 20

US-10-202-062-20
; Sequence 20, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-202-062-20
Query Match 100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYSGIACFLKE 60
QY 61 DSYWDNDDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQNISPLVVRGPQ 120
Db 61 DSYWDNDDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQNISPLVVRGPQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKTYSPDPILLMKSRNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKTYSPDPILLMKSRNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
RESULT 21
US-10-662-431-2
; Sequence 2, Application US/10662431
; Publication No. US20040047864A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,431
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-431-2

Query Match      100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DSYWDPNDEESMNSPCQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DSYWDPNDEESMNSPCQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSDAEYGLY 240
Db 181 FYYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSDAEYGLY 240
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 22
US-10-662-430-2
; Sequence 2, Application US/10662430
; Publication No. US20040048340A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,430
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504

; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-430-2

Query Match      100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DSYWDPNDEESMNSPCQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DSYWDPNDEESMNSPCQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSDAEYGLY 240
Db 181 FYYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSDAEYGLY 240
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 23
US-10-652-244-2
; Sequence 2, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-10-652-244-2

Query Match      100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVYFTNELKQMDKYKSGIACFLKE 60
```

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Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 24
US-10-381-160-5
; Sequence 5, Application US/10381160
; Publication No. US20040131587A1
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING COMBINATION THERAPY
; FILE REFERENCE: 2993-NO
; CURRENT APPLICATION NUMBER: US/10/381,160
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/242,868
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-381-160-5

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 25
US-10-755-889-210
; Sequence 210, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
```

```
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 210
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-210

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 26
US-10-491-326-1
; Sequence 1, Application US/10491326
; Publication No. US20040186051A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: Robert F. Kelley, Stephanie H. Lindstrom
; TITLE OF INVENTION: Apo-2 Ligand Variants and Uses Thereof
; FILE REFERENCE: P1858R1
; CURRENT APPLICATION NUMBER: US/10/491,326
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 60/326,622
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-491-326-1

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
```

Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
Qy 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSRNSCKDAEYGLY 240
Db 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSRNSCKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 27
US-10-810-063-2
; Sequence 2, Application US/10810063
; Publication No. US20040213764A1
; GENERAL INFORMATION:
; APPLICANT: WOLD, WILLIAM
; APPLICANT: TOLLEFSON, ANN
; TITLE OF INVENTION: ADENOVIRUS REPLICATION-COMPETENT VECTORS EXPRESSING
; TITLE OF INVENTION: TRAIL
; FILE REFERENCE: INGN:106US
; CURRENT APPLICATION NUMBER: US/10/810,063
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 60/458,493
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-810-063-2

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCWQVKWLRLVTKMLRTSEETISTVQEKQONISPLVREGRGP 120
Db 61 DDSYWDPNDEESMNSPCWQVKWLRLVTKMLRTSEETISTVQEKQONISPLVREGRGP 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
Qy 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSRNSCKDAEYGLY 240
Db 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSRNSCKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 28
US-10-825-282-22
; Sequence 22, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: 60/134,416

; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-282-22

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCWQVKWLRLVTKMLRTSEETISTVQEKQONISPLVREGRGP 120
Db 61 DDSYWDPNDEESMNSPCWQVKWLRLVTKMLRTSEETISTVQEKQONISPLVREGRGP 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180
Qy 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSRNSCKDAEYGLY 240
Db 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSRNSCKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 29
US-10-825-282-24
; Sequence 24, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-282-24

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Qy 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
```

RESULT 30

```
US-10-399-116-5
; Sequence 5, Application US/10399116
; Publication No. US20040247563A1
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; TITLE OF INVENTION: Method of Enhancing Lymphocyte-Mediated Immune Responses
; FILE REFERENCE: 2995-WO
; CURRENT APPLICATION NUMBER: US/10/399,116
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US 60/245,721
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-116-5

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Qy 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
```

RESULT 31

```
US-10-688-845-36
; Sequence 36, Application US/10688845
; Publication No. US20040247578A1
; GENERAL INFORMATION:
; APPLICANT: Lotze, Michael T
; APPLICANT: Tahara, Hideaki
```

```
; TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
; FILE REFERENCE: UPT-004
; CURRENT APPLICATION NUMBER: US/10/688,845
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,865
; PRIOR FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-688-845-36

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Qy 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
```

RESULT 32

```
US-10-861-685-1
; Sequence 1, Application US/10861685
; Publication No. US20040253708A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/10/861,685
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US/08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-685-1

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
```

Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYDPDPILLMKARNCSKDAEYGLY 240
Db 181 FYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYDPDPILLMKARNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 33

US-10-771-254-1
; Sequence 1, Application US/10771254
; Publication No. US20050020498A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: Flores, Heather
; APPLICANT: Lin, Tanya P.
; APPLICANT: Pai, Roger
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Matthews, Timothy C.
; TITLE OF INVENTION: Apo-2 LIGAND/TRAIL FORMULATIONS
; FILE REFERENCE: P1857R1P1
; CURRENT APPLICATION NUMBER: US/10/771,254
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/338,249
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/US02/36251
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-254-1

Query Match 100.0%; Score 281; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYDPDPILLMKARNCSKDAEYGLY 240
Db 181 FYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYDPDPILLMKARNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 34

US-10-855-559-2
; Sequence 2, Application US/10855559
; Publication No. US20050031593A1
; GENERAL INFORMATION:
; APPLICANT: Harding, Thomas
; APPLICANT: Jooss, Karin
; APPLICANT: Lalani, Alehad
; APPLICANT: Donahue, Brian
; TITLE OF INVENTION: Method for Treating Cancer By Vector-Mediated Delivery of
; One or More Anti-Angiogenic or Proapoptotic Genes

; FILE REFERENCE: 3802-094-27
; CURRENT APPLICATION NUMBER: US/10/855,559
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/475,006
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-855-559-2

Query Match 100.0%; Score 281; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYDPDPILLMKARNCSKDAEYGLY 240
Db 181 FYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYDPDPILLMKARNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 35

US-10-451-200-5
; Sequence 5, Application US/10451200
; Publication No. US20050048645A1
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; TITLE OF INVENTION: METHOD OF TREATING OR PREVENTING DISEASE CHARACTERIZED BY CRYPTOC
; TITLE OF INVENTION: NEOFORMANS INFECTION
; FILE REFERENCE: 2966-WO
; CURRENT APPLICATION NUMBER: US/10/451,200
; CURRENT FILING DATE: 2003-06-21
; PRIOR APPLICATION NUMBER: US 60/259,653
; PRIOR FILING DATE: 2001-01-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-200-5

Query Match 100.0%; Score 281; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180

Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVVIHEKG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 36

US-10-495-353-1

; Sequence 1, Application US/10495353
; Publication No. US200508006A1
; GENERAL INFORMATION:
; APPLICANT: FLORES, Heather
; APPLICANT: LIN, Tanya P.
; APPLICANT: PAI, Roger
; APPLICANT: SHAHROKH, Zahra
; APPLICANT: MATTHEWS, Timothy
; TITLE OF INVENTION: Apo-2 LIGAND/TRAIL FORMULATIONS
; FILE REFERENCE: P1857R1
; CURRENT APPLICATION NUMBER: US/10/495,353
; CURRENT FILING DATE: 2004-05-12
; PRIOR FILING DATE: PCT/US02/36251
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/338,249
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-495-353-1

Query Match 100.0%; Score 281; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVVIHEKG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 37

US-10-652-979-1

; Sequence 1, Application US/10652979
; Publication No. US20050809958A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Schwalli, Ralph H.
; TITLE OF INVENTION: Apo-2 Ligand
; FILE REFERENCE: P0578P3C1
; CURRENT APPLICATION NUMBER: US/10/652,979
; CURRENT FILING DATE: 2003-08-29
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 09/060,533

; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: US 09/007,886
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 08/780,496
; PRIOR FILING DATE: 1997-01-08
; PRIOR APPLICATION NUMBER: US 60/009,755
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-979-1
Query Match 100.0%; Score 281; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDNDDESMNSPCQVQWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVVIHEKG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 38

US-10-066-209-3

; Sequence 3, Application US/10066209
; Publication No. US20020115110A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030-D1
; CURRENT APPLICATION NUMBER: US/10/066,209
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 03/072,993
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-066-209-3
Query Match 99.3%; Score 279; DB 13; Length 279;
Best Local Similarity 100.0%; Pred. No. 6.3e-270;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MMEVQGGPSLGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKEDD 62
|||

Db 1 MMEVQGGPSLQGTCTVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGKIACFLKEDD 60
Qy 63 SYWDNDDEESMNSPCQVQKQRLQRLVRKMLILTSSETISTVQEKQONISPLVRERGPQV 122
Db 61 SYWDNDDEESMNSPCQVQKQRLQRLVRKMLILTSSETISTVQEKQONISPLVRERGPQV 120
Qy 123 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 182
Db 121 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
Qy 183 YIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWCKDAEYGLYSI 242
Db 181 YIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWCKDAEYGLYSI 240
Qy 243 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279

RESULT 39

US-10-738-423-10
; Sequence 10, Application US/10738423
; Publication No. US20040229338A1
; GENERAL INFORMATION:
; APPLICANT: Bermudes, G.
; APPLICANT: King, I.
; APPLICANT: Clairmont, C.
; APPLICANT: Lin, S.
; APPLICANT: Belcourt, M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 8002-059
; CURRENT APPLICATION NUMBER: US/10/738,423
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US/09/645,415
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/157,581
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/157,637
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion construct
US-10-738-423-10

Query Match 86.1%; Score 242; DB 16; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.5e-233;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 40 NELKQMDKYSGKIACFLKEDDSYWDNDDEESMNSPCQVQKQRLQRLVRKMLILTSSET 99
Db 25 NELKQMDKYSGKIACFLKEDDSYWDNDDEESMNSPCQVQKQRLQRLVRKMLILTSSET 84
Qy 100 ISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRS 159
Db 85 ISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRS 144
Qy 160 GHSFSLNHLRNGELVIEHKGFIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDP 219
Db 145 GHSFSLNHLRNGELVIEHKGFIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDP 204
Qy 220 ILLMKSARNCSWCKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFL 279
Db 205 ILLMKSARNCSWCKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFL 264
Qy 280 VG 281
Db 265 VG 266

RESULT 40

US-10-367-094-22
; Sequence 22, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-094-22

Query Match 84.7%; Score 238; DB 16; Length 279;
Best Local Similarity 100.0%; Pred. No. 5.7e-229;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLQGTCTVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGKIACFLKE 60
Db 1 MAMMEVQGGPSLQGTCTVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGKIACFLKE 60
Qy 61 DDSYWDNDDEESMNSPCQVQKQRLQRLVRKMLILTSSETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDNDDEESMNSPCQVQKQRLQRLVRKMLILTSSETISTVQEKQONISPLVRERGPQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWCKDAEY 238
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWCKDAEY 238

RESULT 41

US-09-855-544A-16
; Sequence 16, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 27866-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-16

Query Match 68.7%; Score 193; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.9e-184;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLQGTCTVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGKIACFLKE 60
Db 1 MAMMEVQGGPSLQGTCTVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGKIACFLKE 60
Qy 61 DDSYWDNDDEESMNSPCQVQKQRLQRLVRKMLILTSSETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDNDDEESMNSPCQVQKQRLQRLVRKMLILTSSETISTVQEKQONISPLVRERGPQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180

```
Db 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
Qy 181 FYIYSQTYFRFQ 193
Db 181 FYIYSQTYFRFQ 193

RESULT 42
US-10-652-244-11
; Sequence 11, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-10-652-244-11

Query Match 66.5%; Score 187; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.5e-178;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSEETISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
Db 67 TSEETISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 126

Qy 155 ESSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQIYKYT 214
Db 127 ESSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQIYKYT 186

Qy 215 SYDPILLMKSAKNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 187 SYDPILLMKSAKNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246

Qy 275 FGAFLVG 281
Db 247 FGAFLVG 253

RESULT 43
US-10-652-244-13
; Sequence 13, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-10-652-244-11

Query Match 66.5%; Score 187; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.5e-178;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSEETISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
Db 67 TSEETISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 126

Qy 155 ESSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQIYKYT 214
Db 127 ESSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQIYKYT 186

Qy 215 SYDPILLMKSAKNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 187 SYDPILLMKSAKNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246

Qy 275 FGAFLVG 281
Db 247 FGAFLVG 253

RESULT 44
US-10-723-003-66
; Sequence 66, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-66

Query Match 66.5%; Score 187; DB 16; Length 400;
Best Local Similarity 100.0%; Pred. No. 6.8e-178;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

95	Qy	TSEETISTVQSKQKQNI	SPLVRRG	QORVA	AAHTG	TRGRS	NTLSS	PNKS	NKVE	KALGR	KIN	SW	154
214	Db	TSEETISTVQSKQKQNI	SPLVRRG	QORVA	AAHTG	TRGRS	NTLSS	PNKS	NKVE	KALGR	KIN	SW	273
155	Qy	ESSRSGHS	FLNLH	RGELV	THE	KGFY	YSQTY	FRQ	EEIK	ENT	KDQ	KV	214
274	Db	ESSRSGHS	FLNLH	RGELV	THE	KGFY	YSQTY	FRQ	EEIK	ENT	KDQ	KV	333
215	Qy	SYPPDILL	MKSAR	NSCW	KDAEY	GLYS	IYQGG	IFEL	KEND	RI	FVS	VTNE	274
334	Db	SYPPDILL	MKSAR	NSCW	KDAEY	GLYS	IYQGG	IFEL	KEND	RI	FVS	VTNE	393
275	Qy	FGAFLVG	281										
394	Db	FGAFLVG	400										

```

RESULT 45
US-10-389-223A-6
; Sequence 6, Application US/10389223A
; Publication No. US20040033511A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wajant, Harald
; APPLICANT: Wuest, Thomas
; APPLICANT: Moosmayer, Dieter
; TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytoki
; TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
; FILE REFERENCE: 1708.002U51
; CURRENT APPLICATION NUMBER: US/10/389,223A
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of sequence 6: synthetic amino acid sequence of an
; OTHER INFORMATION: anti-body-cytokine AMAIZE fusion protein of the invention exempli
; OTHER INFORMATION: TRAIL-AMAIZE (40)
; FEATURE:
; OTHER INFORMATION: Stop codon: NT 1384-1386
; US-10-389-223A-6

```

RESULT 46
US-10-389-223A-4
; Sequence 4, Application US/10389223A
; Publication No. US20040033511A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wajant, Harald

```

? APPLICANT: Muest, Thomas
? APPLICANT: Moosmayer, Dieter
? TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytokir
? TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
? FILE OF INVENTION: AMAIZE
? FILE REFERENCE: 1708.002US1
? CURRENT APPLICATION NUMBER: US/10/389,223A
? CURRENT FILING DATE: 2003-03-14
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 4
? LENGTH: 480
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of sequence 4: synthetic amino acid sequence of an
? OTHER INFORMATION: anti-body-cytokine AMAIZE fusion protein of the invention exemplif
? OTHER INFORMATION: TRAIL-AMAIZE (OS4)
? FEATURE:
? OTHER INFORMATION: Stop codon: NT 1441-1443
? US-10-389-223A-4

```

RESULT 47
US-10-389-223A-2
Sequence 2, Application US/10389223A
Publication No. US20040033511A1
GENERAL INFORMATION:
APPLICANT: Pfizenmaier, Klaus
APPLICANT: Wajant, Harald
APPLICANT: Wuest, Thomas
APPLICANT: Moosmayer, Dieter
TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytokir
TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
FILE REFERENCE: 1708.002US1
CURRENT APPLICATION NUMBER: US/10/389, 223A
CURRENT FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 614
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of sequence 2: synthetic amino acid sequence of an
OTHER INFORMATION: anti-body-cytokine AMAIZE fusion protein of the invention exemplifi
OTHER INFORMATION: TRAIL-AMAIZE (MBOS4)
FEATURE:
OTHER INFORMATION: Stop codon: NT 1843-1845
US-10-389-223A-2

Query Match 66.5%; Score 187; DB 15; Length 614;
Best Local Similarity 100.0%; Pred. No. 9.9e-178;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSETISTVQKQONISPLVRERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 154
|
Db 428 TSETISTVQKQONISPLVRERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 487
|
Qy 155 ESSRSKSHFLNLHLRNGELVIHKGFFYYISQTYFRFOBEIKENTKNDKQMVQYIYKYT 214
|
Db 488 ESSRSKSHFLNLHLRNGELVIHKGFFYYISQTYFRFOBEIKENTKNDKQMVQYIYKYT 547
|
Qy 215 SYPPILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
|
Db 548 SYPPILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 607
|
Qy 275 FGAFLVG 281
|
Db 608 FGAFLVG 614
|

RESULT 48
US-09-900-530A-10
; Sequence 10, Application US/09900530A
; Patent No. US20020128438A1
; GENERAL INFORMATION:
; APPLICANT: Seol, Dae-Wu
; APPLICANT: Billiar, Timothy R.
; TITLE OF INVENTION: DNA Cassette for the Production of
; TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline
; TITLE OF INVENTION: /doxycycline-Inducible Adeno-Associated Virus Vector, Their
; TITLE OF INVENTION: Combination and Use in Gene Therapy
; FILE REFERENCE: 5006-1-002
; CURRENT APPLICATION NUMBER: US/09/900.530A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: KR 2000-38441
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 168
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-900-530A-10

Query Match 59.8%; Score 168; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 3e-159;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 VRERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 173
|
Db 1 VRERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 60
|
Qy 174 LVIHEKGFYYISQTYFRFOBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWK 233
|
Db 61 LVIHEKGFYYISQTYFRFOBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWK 120
|
Qy 234 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 281
|
Db 121 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 168
|

RESULT 49
US-10-981-989-14
; Sequence 14, Application US/10981989
; Publication No. US20050113328A1
; GENERAL INFORMATION:
; APPLICANT: Devi, Gayathri
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Method and Antisense Compound for Potentiating Anti-Cancer Agents
; FILE REFERENCE: 50450.8058.US00
; CURRENT APPLICATION NUMBER: US/10/981.989
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,139
; PRIOR FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-981-989-14

Query Match 59.8%; Score 168; DB 17; Length 168;
Best Local Similarity 100.0%; Pred. No. 3e-159;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 VRERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 173
|
Db 1 VRERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 60
|
Qy 174 LVIHEKGFYYISQTYFRFOBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWK 233
|
Db 61 LVIHEKGFYYISQTYFRFOBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWK 120
|
Qy 234 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 281
|
Db 121 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 168
|

RESULT 50
US-10-855-559-4
; Sequence 4, Application US/10855559
; Publication No. US20050031593A1
; GENERAL INFORMATION:
; APPLICANT: Harding, Thomas
; APPLICANT: Jooss, Karin
; APPLICANT: Lalani, Alshad
; APPLICANT: Donahue, Brian
; TITLE OF INVENTION: Method for Treating Cancer By Vector-Mediated Delivery of
; TITLE OF INVENTION: One or More Anti-Angiogenic or Proapoptotic Genes
; FILE REFERENCE: 3802-094-27
; CURRENT APPLICATION NUMBER: US/10/855,559
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/475,006
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-855-559-4

Query Match 59.8%; Score 168; DB 17; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.9e-159;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 VRERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 173
|
Db 61 VRERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 120
|
Qy 174 LVIHEKGFYYISQTYFRFOBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWK 233
|
Db 121 LVIHEKGFYYISQTYFRFOBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWK 180
|
Qy 234 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 281
|
Db 181 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 228
|

RESULT 51
US-10-723-003-64
; Sequence 64, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF

;; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS

;; FILE REFERENCE: 549062000200

;; CURRENT APPLICATION NUMBER: US/10/723,003

;; CURRENT FILING DATE: 2003-11-26

;; PRIOR APPLICATION NUMBER: CN 2003101199300

;; PRIOR FILING DATE: 2003-11-25

;; PRIOR APPLICATION NUMBER: CN 031292909

;; PRIOR FILING DATE: 2003-06-13

;; NUMBER OF SEQ ID NOS: 68

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 64

;; LENGTH: 365

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Synthetic Construct

US-10-723-003-64

Query Match 59.8%; Score 168; DB 16; Length 365;

Best Local Similarity 100.0%; Pred. No. 6e-159;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 VRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 173

DB 198 VRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 257

QY 174 LVIEHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSWSK 233

DB 258 LVIEHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSWSK 317

QY 234 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

DB 318 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 365

RESULT 52

US-10-723-003-68

;; Sequence 68, Application US/10723003

;; Publication No. US20040254108A1

;; GENERAL INFORMATION:

;; APPLICANT: MA, Jing

;; APPLICANT: GUO, Yajun

;; TITLE OF INVENTION: PREPARATION AND APPLICATION OF

;; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS

;; FILE REFERENCE: 549062000200

;; CURRENT APPLICATION NUMBER: US/10/723,003

;; CURRENT FILING DATE: 2003-11-26

;; PRIOR APPLICATION NUMBER: CN 2003101199300

;; PRIOR FILING DATE: 2003-11-25

;; PRIOR APPLICATION NUMBER: CN 031292909

;; PRIOR FILING DATE: 2003-06-13

;; NUMBER OF SEQ ID NOS: 68

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 68

;; LENGTH: 582

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Synthetic Construct

US-10-723-003-68

Query Match 59.8%; Score 168; DB 16; Length 582;

Best Local Similarity 100.0%; Pred. No. 9e-159;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 VRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 173

DB 415 VRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 474

QY 174 LVIEHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSWSK 233

DB 475 LVIEHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSWSK 534

QY 234 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

DB 535 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 582

RESULT 53

US-09-779-050A-16

;; Sequence 16, Application US/09779050A

;; Patent No. US20020160416A1

;; GENERAL INFORMATION:

;; APPLICANT: BOYLE, WILLIAM

;; APPLICANT: HSU, HAILING

;; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY

;; FILE REFERENCE: A-570B

;; CURRENT APPLICATION NUMBER: US/09/779,050A

;; CURRENT FILING DATE: 2001-02-12

;; PRIOR APPLICATION NUMBER: 60/181,800

;; PRIOR FILING DATE: 2000-02-11

;; NUMBER OF SEQ ID NOS: 52

;; SOFTWARE: PatentIn version 3.0

;; SEQ ID NO 16

;; LENGTH: 166

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-09-779-050A-16

Query Match

Best Local Similarity 59.1%; Score 166; DB 9; Length 166;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 ERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 175

DB 1 ERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 60

QY 176 IHEKGFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSWSKDA 235

DB 61 IHEKGFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSWSKDA 120

QY 236 EYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

DB 121 EYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 166

RESULT 54

US-10-216-074-7

;; Sequence 7, Application US/10216074

;; Publication No. US20030148445A1

;; GENERAL INFORMATION:

;; APPLICANT: Shu, Hong-Bing

;; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

;; FILE REFERENCE: 2879-72

;; CURRENT APPLICATION NUMBER: US/10/216,074

;; PRIOR FILING DATE: 2003-03-12

;; PRIOR APPLICATION NUMBER: US/09/565,423

;; PRIOR FILING DATE: 2000-05-05

;; PRIOR APPLICATION NUMBER: UNKNOWN

;; PRIOR FILING DATE: 2000-05-01

;; PRIOR APPLICATION NUMBER: 60/132,892

;; PRIOR FILING DATE: 1999-05-06

;; NUMBER OF SEQ ID NOS: 17

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 7

;; LENGTH: 161

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-10-216-074-7

Query Match

Best Local Similarity 57.3%; Score 161; DB 14; Length 161;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV IHEKG 180

```
Db 1 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEK 60
Qy 181 FYIYISQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGL 240
Db 61 FYIYISQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGL 120
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 281
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 55
US-10-338-083-11
; Sequence 11, Application US/10338083
; Publication No. US2003016659A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Basell I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-11

Query Match 57.3%; Score 161; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.9e-152;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 QVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEK 179
Db 1 QVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEK 60

Qy 180 GFYIYISQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGL 239
Db 61 GFYIYISQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGL 120

Qy 240 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 56
US-10-611-399-11
; Sequence 11, Application US/10611399
; Publication No. US20040170602A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Basell I.
; TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
; FILE REFERENCE: A-71273-3
; CURRENT APPLICATION NUMBER: US/10/611,399
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-611-399-11

Query Match 57.3%; Score 161; DB 16; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.9e-152;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 QVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEK 179
Db 1 QVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEK 60

Qy 180 GFYIYISQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGL 239
Db 61 GFYIYISQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGL 120

Qy 240 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 57
US-10-794-751-11
; Sequence 11, Application US/10794751
; Publication No. US20050048626A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Thomason, Adam Read
; APPLICANT: Zhukovsky, Eugene Alexander
; TITLE OF INVENTION: BAFF VARIANTS AND METHODS THEREOF
; FILE REFERENCE: A-72175-1
; CURRENT APPLICATION NUMBER: US/10/794,751
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/452,707
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/482,081
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 60/523,880
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US 60/528,104
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-751-11

Query Match 57.3%; Score 161; DB 17; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.9e-152;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 QVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEK 179
Db 1 QVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEK 60

Qy 180 GFYIYISQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGL 239
Db 61 GFYIYISQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGL 120

Qy 240 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 58
US-10-778-890-10
; Sequence 10, Application US/10778890
```

```
; Publication No. US20050112596A1
; GENERAL INFORMATION:
; APPLICANT: TSCHOPP, JURG
; TITLE OF INVENTION: APRIL-A NOVEL PROTEIN WITH GROWTH EFFECTS
; FILE REFERENCE: A049 US
; CURRENT APPLICATION NUMBER: US/10/778,890
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: US/09/520,489
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/19191
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/079,384
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/058,786
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-778-890-10

Query Match      56.2%; Score 158; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 2.8e-149;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHKGFPY 182
DB 1 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHKGFPY 60

QY 183 YIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSAARNCSWCKDAEYGLYSI 242
DB 61 YIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSAARNCSWCKDAEYGLYSI 120

QY 243 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPFLV 280
DB 121 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPFLV 158

RESULT 59
US-10-185-425-5
; Sequence 5, Application US/10185425
; Publication No. US20030053984A1
; GENERAL INFORMATION:
; APPLICANT: Apotech Research and Development Ltd.
; APPLICANT: Techopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Holler, Nils
; TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
; FILE REFERENCE: 1708.001US1
; CURRENT APPLICATION NUMBER: US/10/185,425
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: PCT/EP00/13032
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: DE 199 63 859.4
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TRAIL-ACRP30
; NAME/KEY: DOMAIN
; LOCATION: (1)...(8)
; OTHER INFORMATION: Flag
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (9)...(16)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (17)...(108)
; OTHER INFORMATION: mouseACRP30 aa 18-111
; FEATURE:
```

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; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (17)...(108)
; OTHER INFORMATION: mouseACRP30 aa 18-111
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (109)...(110)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (111)...(296)
; OTHER INFORMATION: humanTRAIL aa 95-281
US-10-185-425-5

Query Match      55.5%; Score 156; DB 14; Length 296;
Best Local Similarity 100.0%; Pred. No. 4.8e-147;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 ITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHKGFPYIY 185
DB 141 ITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHKGFPYIY 200

QY 186 SOTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSAARNCSWCKDAEYGLYSIYQ 245
DB 201 SOTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSAARNCSWCKDAEYGLYSIYQ 260

QY 246 GIFELKENDRIFVSVTNEHLIDMDHEASFFGAPFLV 281
DB 261 GIFELKENDRIFVSVTNEHLIDMDHEASFFGAPFLV 296

RESULT 60
US-10-871-776-5
; Sequence 5, Application US/10871776
; Publication No. US20040235117A1
; GENERAL INFORMATION:
; APPLICANT: Apotech Research and Development Ltd.
; APPLICANT: Techopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Holler, Nils
; TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
; FILE REFERENCE: 1708.001US1
; CURRENT APPLICATION NUMBER: US/10/871,776
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/10/185,425
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: PCT/EP00/13032
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: DE 199 63 859.4
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TRAIL-ACRP30
; NAME/KEY: DOMAIN
; LOCATION: (1)...(8)
; OTHER INFORMATION: Flag
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (9)...(16)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (17)...(108)
; OTHER INFORMATION: mouseACRP30 aa 18-111
; FEATURE:
```

```
; NAME/KEY: DOMAIN
; LOCATION: (109)...(110)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (111)...(296)
; OTHER INFORMATION: humanTRAIL aa 95-281
US-10-871-776-5

Query Match      55.5%; Score 156; DB 16; Length 296;
Best Local Similarity 100.0%; Pred. No. 4.8e-147; Indels 0; Gaps 0;
Matches 156; Conservative 0; Mismatches 0;

Qy 126 ITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKGFYIY 185
Db 141 ITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKGFYIY 200
Qy 186 SQTFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLYSIYQG 245
Db 201 SQTFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLYSIYQG 260
Qy 246 GIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 261 GIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 296

RESULT 61
US-10-781-866-29
; Sequence 29, Application US/10781866
; Publication No. US20040258681A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/10/781,866
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/569,611
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-866-29

Query Match      50.2%; Score 141; DB 16; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.8e-132; Indels 0; Gaps 0;
Matches 141; Conservative 0; Mismatches 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60
Db 25 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 84
Qy 61 DDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONI SPLVRERGQP 120
Db 85 DDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQP 144
Qy 121 RVAAHITGTRGRNTLSSPNS 141
Db 145 RVAAHITGTRGRNTLSSPNS 165

RESULT 62
US-09-855-544A-13
; Sequence 13, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-13

Query Match      50.2%; Score 141; DB 9; Length 246;
Best Local Similarity 100.0%; Pred. No. 3.9e-132; Indels 0; Gaps 0;
Matches 141; Conservative 0; Mismatches 0;

Qy 141 SKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKGFYIYQTYFRFQBEIKENT 200
Db 106 SKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKGFYIYQTYFRFQBEIKENT 165
Qy 201 KNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 260
Db 166 KNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 225
Qy 261 TNEHLIDMDHEASFFGAFLVG 281
Db 226 TNEHLIDMDHEASFFGAFLVG 246

RESULT 63
US-10-781-866-30
; Sequence 30, Application US/10781866
; Publication No. US20040258681A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/10/781,866
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/569,611
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-866-30

Query Match      47.7%; Score 134; DB 16; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.2e-125; Indels 0; Gaps 0;
Matches 134; Conservative 0; Mismatches 0;

Qy 112 PLVREGRQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRN 171
Db 122 PLVREGRQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRN 181
Qy 172 GELVHEKGFYIYQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCW 231
Db 182 GELVHEKGFYIYQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCW 241
Qy 232 SKDAEYGLYSIYQG 245
Db 242 SKDAEYGLYSIYQG 255

RESULT 64
US-10-978-203-23
; Sequence 23, Application US/10978203
; Publication No. US20050112666A1
; GENERAL INFORMATION:
; APPLICANT: Chicheportiche, Yves
; APPLICANT: Browning, Jeffrey
; TITLE OF INVENTION: Tumor Necrosis Factor Related Ligand
; FILE REFERENCE: A003
; CURRENT APPLICATION NUMBER: US/10/978,203
; CURRENT FILING DATE: 2004-10-29
```



```

; PRIOR APPLICATION NUMBER: 60/023,541
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: 60/028,515
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: 60/040,820
; PRIOR FILING DATE: 1997-03-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 283
; TYPE: PRT
; ORGANISM: homo sapien
US-10-978-203-23

Query Match
Best Local Similarity 46.3%; Score 130; DB 17; Length 283;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 MOVKQLRQLVKMLRTSEETISTVQEKQKNISPLVRRGQORVAAHITGTRGSNTLS 137
DB 82 MOVKQLRQLVKMLRTSEETISTVQEKQKNISPLVRRGQORVAAHITGTRGSNTLS 141
QY 138 SPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQBEIK 197
DB 142 SPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQBEIK 201
QY 198 ENTNKDKQMV 207
DB 202 ENTNKDKQMV 211

RESULT 65
US-10-978-131-23
; Sequence 23, Application US/10978131
; Publication No. US20050118629A1
; GENERAL INFORMATION:
; APPLICANT: Chicheportiche, Yves
; APPLICANT: Browning, Jeffrey
; TITLE OF INVENTION: Tumor Necrosis Factor Related Ligand
; FILE REFERENCE: A003
; CURRENT APPLICATION NUMBER: US/10/978,131
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/023,541
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: 60/028,515
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: 60/040,820
; PRIOR FILING DATE: 1997-03-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 283
; TYPE: PRT
; ORGANISM: homo sapien
US-10-978-131-23

Query Match
Best Local Similarity 46.3%; Score 130; DB 17; Length 283;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 MOVKQLRQLVKMLRTSEETISTVQEKQKNISPLVRRGQORVAAHITGTRGSNTLS 137
DB 82 MOVKQLRQLVKMLRTSEETISTVQEKQKNISPLVRRGQORVAAHITGTRGSNTLS 141
QY 138 SPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQBEIK 197
DB 142 SPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQBEIK 201
QY 198 ENTNKDKQMV 207
DB 202 ENTNKDKQMV 211
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RESULT 66
US-10-116-378-29
; Sequence 29, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/116,378
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 29
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-29

Query Match
Best Local Similarity 45.2%; Score 127; DB 13; Length 164;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 GPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTH 177
DB 1 GPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTH 60
QY 178 EKGFIYYSQTYFRQBEIKENTKNDKQMVQIYKYTSYPPDILLMKARNSCWSKDABY 237
DB 61 EKGFIYYSQTYFRQBEIKENTKNDKQMVQIYKYTSYPPDILLMKARNSCWSKDABY 120
QY 238 GLYSIQ 244
DB 121 GLYSIQ 127

RESULT 67
US-10-959-537-29
; Sequence 29, Application US/10959537
; Publication No. US20050069983A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/959,537
; CURRENT FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US/09/247,225
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 29
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-537-29

Query Match
Best Local Similarity 45.2%; Score 127; DB 17; Length 164;
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	Best Local Similarity	100.0%; Pred. No. 2.7e-118;	Mismatches 0; Indels 0; Gaps 0
	Matches 127; Conservative		
Qy	118	GPOVAAHITCRGRSNTLSSPNSKNEALGKINSWESSBGSHSFSLNHLRNGELVIH	177
Dd	1	GPOVAAHITCRGRSNTLSSPNSKNEALGKINSWESSBGSHSFSLNHLRNGELVIH	60
Qy	178	EKGFWIYSQYFRFQEIEIKENTKNDKMVOYIYKYTSYPDPILLMKARNCSWKDAEY	237
Dd	61	EKGFWIYSQYFRFQEIEIKENTKNDKMVOYIYKYTSYPDPILLMKARNCSWKDAEY	120
Qy	238	GLYSIQY 244	
Dd	121	GLYSIQY 127	

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RESULT 68
US-10-006-305A-8
; Sequence 8, Application US/10006305A
; Publication No. US20050048476A1
; GENERAL INFORMATION:
; APPLICANT: PRUSSAK, CHARLES E.
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: CANTWELL, MARK J.
; TITLE OF INVENTION: NOVEL CHIMERIC TNF LIGANDS
; FILE REFERENCE: 041673-2092
; CURRENT APPLICATION NUMBER: US/10/006,305A
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFA
; OTHER INFORMATION: polypeptide encoded by the DNA sequence of SEQ ID NO:4
US-10-006-305A-8

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RESULT 69
US-09-855-544A-15
; Sequence 15, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855.544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-15

Qy	1	MAMMEVGGPSSIGOTCVLIVIFETVLLOSICVAVTVVYFTELKOMODKYKSGGIACFLKE	60
Db	1	MAMMEVGGPSSIGOTCVLIVIFETVLLOSICVAVTVVYFTELKOMODKYKSGGIACFLKE	60
Qy	61	DDSYDNDPDEESNMSPCWQVKWQLRQVKMLRTSEETISVQBEKQ	107
Db	61	DDSYDNDPDEESNMSPCWQVKWQLRQVKMLRTSEETISVQBEKQ	107

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RESULT 70
US-09-855-544A-14
; Sequence 14, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-14

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RESULT 71
US-09-855-544A-10
; Sequence 10, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-10

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RESULT 72

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US-10-367-094-20
; Sequence 20, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-094-20

Query Match          32.0%; Score 90; DB 16; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.5e-81;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

RESULT 73
US-10-652-244-4
; Sequence 4, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
US-10-652-244-4

Query Match          32.0%; Score 90; DB 15; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.6e-81;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

US-10-662-429-2.oligo.rapb
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US-10-781-866-32
; Sequence 32, Application US/10781866
; Publication No. US20040258681A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/10/781,866
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/569,611
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-866-32

Query Match          32.0%; Score 90; DB 16; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.8e-81;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 25 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 84
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
DB 85 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 114

RESULT 75
US-10-781-866-31
; Sequence 31, Application US/10781866
; Publication No. US20040258681A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/10/781,866
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/569,611
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-866-31

Query Match          32.0%; Score 90; DB 16; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e-81;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 25 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 84
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
DB 85 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 114

Search completed: June 22, 2005, 07:05:30
Job time : 165 secs
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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:39:23 ; Search time 42 Seconds
(without alignments)
499.438 Million cell updates/sec

Title: US-10-662-429-2
Perfect score: 281
Sequence: 1 MAMVEQGSPSLGQTCVLIV.....NEHLIDMDHEASFFGAFIVG 281

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	281	100.0	281	1	US-08-670-354-2
2	281	100.0	281	3	US-08-584-031-1
3	281	100.0	281	3	US-08-780-496-1
4	281	100.0	281	3	US-08-883-086-10
5	281	100.0	281	3	US-09-320-424-2
6	281	100.0	281	3	US-09-333-593A-6
7	281	100.0	281	4	US-09-157-864-11
8	281	100.0	281	4	US-09-825-563-2
9	281	100.0	281	4	US-09-919-039-118
10	281	100.0	281	4	US-09-582-450-1
11	281	100.0	281	4	US-09-934-465-1
12	281	100.0	281	4	US-10-011-125A-4
13	281	100.0	281	5	PCT-US96-10895-2
14	279	99.3	279	3	US-09-072-993C-3
15	187	66.5	253	3	US-09-320-424-11
16	187	66.5	253	4	US-09-825-563-11
17	187	66.5	256	3	US-09-320-424-13
18	187	66.5	256	4	US-09-825-563-13
19	174	61.9	177	3	US-09-105-343A-7
20	161	57.3	161	4	US-09-565-423-7
21	141	50.2	169	4	US-09-569-611C-29
22	134	47.7	271	4	US-09-569-611C-30
23	103	36.7	121	4	US-09-513-999C-7833
24	90	32.0	101	1	US-08-670-354-4
25	90	32.0	101	3	US-09-320-424-4
26	90	32.0	101	4	US-09-825-563-4
27	90	32.0	101	5	PCT-US96-10895-4
28	90	32.0	90	28	Sequence 2, Appli
29	90	32.0	90	29	Sequence 1, Appli
30	85	30.2	85	4	Sequence 1, Appli
31	24	8.5	24	4	Sequence 10, Appli
32	15	5.3	15	4	Sequence 2, Appli
33	15	5.3	15	4	Sequence 6, Appli
34	15	5.3	15	4	Sequence 11, Appli
35	14	5.0	14	4	Sequence 2, Appli
36	14	5.0	14	4	Sequence 118, Appli
37	14	5.0	14	4	Sequence 1, Appli
38	14	5.0	14	4	Sequence 1, Appli
39	12	4.3	87	4	Sequence 13, Appli
40	8	2.8	70	4	Sequence 6, Appli
41	7	2.5	96	4	Sequence 13, Appli
42	7	2.5	132	4	Sequence 2, Appli
43	7	2.5	132	4	Sequence 5589, Ap
44	7	2.5	132	4	Sequence 5590, Ap
45	7	2.5	132	4	Sequence 5591, Ap
46	7	2.5	172	3	Sequence 5649, Ap
47	7	2.5	209	4	Sequence 8, Appli
48	7	2.5	209	4	Sequence 24, Appli
49	7	2.5	240	4	Sequence 2, Appli
50	7	2.5	274	4	Sequence 7595, Ap
51	7	2.5	384	4	Sequence 35447, A
52	7	2.5	384	4	Sequence 50664, A
53	7	2.5	429	4	Sequence 186, App
54	7	2.5	432	4	Sequence 189, App
55	7	2.5	487	4	Sequence 173, App
56	7	2.5	554	4	Sequence 18251, A
57	7	2.5	628	4	Sequence 6, Appli
58	7	2.5	645	4	Sequence 183, App
59	7	2.5	700	4	Sequence 11022, A
60	7	2.5	1532	4	Sequence 34, Appli
61	7	2.5	1574	4	Sequence 62, Appli
62	7	2.5	1978	4	Sequence 179, App
63	7	2.5	2071	3	Sequence 60, Appli
64	6	2.1	6	4	Sequence 6, Appli
65	6	2.1	10	4	Sequence 13, Appli
66	6	2.1	24	4	Sequence 31, Appli
67	6	2.1	25	4	Sequence 26, Appli
68	6	2.1	28	4	Sequence 57665, A
69	6	2.1	46	3	Sequence 50, Appli
70	6	2.1	54	4	Sequence 268, App
71	6	2.1	62	4	Sequence 42298, A
72	6	2.1	62	4	Sequence 6548, A
73	6	2.1	76	4	Sequence 7381, Ap
74	6	2.1	76	4	Sequence 32209, A
75	6	2.1	78	4	Sequence 27194, A
76	6	2.1	78	4	Sequence 5502, Ap
77	6	2.1	83	4	Sequence 3425, Ap
78	6	2.1	84	4	Sequence 5440, Ap
79	6	2.1	85	4	Sequence 4910, Ap
80	6	2.1	87	4	Sequence 26098, A
81	6	2.1	88	4	Sequence 5745, Ap
82	6	2.1	88	4	Sequence 59036, A
83	6	2.1	95	4	Sequence 5744, Ap
84	6	2.1	104	3	Sequence 42379, A
85	6	2.1	105	4	Sequence 99, Appli
86	6	2.1	106	2	Sequence 8267, Ap
87	6	2.1	106	2	Sequence 4, Appli
88	6	2.1	106	4	Sequence 4, Appli
89	6	2.1	106	4	Sequence 4, Appli
90	6	2.1	106	5	Sequence 10, Appli
91	6	2.1	106	5	Sequence 4, Appli
92	6	2.1	108	4	Sequence 38247, A
93	6	2.1	108	4	Sequence 53464, A
94	6	2.1	111	4	Sequence 38147, A
95	6	2.1	111	4	Sequence 39454, A
96	6	2.1	111	4	Sequence 53664, A
97	6	2.1	111	4	Sequence 54671, A
98	6	2.1	112	4	Sequence 33124, A
99	6	2.1	112	4	Sequence 48341, A
100	6	2.1	114	4	Sequence 5266, Ap

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Sequence 18251, A
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Sequence 11022, A
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Sequence 179, App
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Sequence 26, Appli
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Sequence 7381, Ap
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Sequence 5502, Ap
Sequence 3425, Ap
Sequence 5440, Ap
Sequence 4910, Ap
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Sequence 5745, Ap
Sequence 59036, A
Sequence 5744, Ap
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Sequence 8267, Ap
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Sequence 53464, A
Sequence 38147, A
Sequence 39454, A
Sequence 53664, A
Sequence 54671, A
Sequence 33124, A
Sequence 48341, A
Sequence 5266, Ap

ALIGNMENTS

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RESULT 1
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cycokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

Query Match      100.0%; Score 281; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAMMEVQGPSLGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Db      1 MAMMEVQGPSLGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Qy      61 DDSYWDNDPDESMNSPCQVQKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGQ 120
Db      61 DDSYWDNDPDESMNSPCQVQKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGQ 120
Qy      121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHGK 180
Db      121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHGK 180
Qy      181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWKADEYGLY 240
Db      181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWKADEYGLY 240
Qy      181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWKADEYGLY 240
Db      181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWKADEYGLY 240
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Qy      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
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RESULT 2
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1
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Query Match      100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAMMEVQGPSLGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Db      1 MAMMEVQGPSLGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Qy      61 DDSYWDNDPDESMNSPCQVQKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGQ 120
Db      61 DDSYWDNDPDESMNSPCQVQKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGQ 120
Qy      121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHGK 180
Db      121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHGK 180
Qy      181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWKADEYGLY 240
Db      181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWKADEYGLY 240
Qy      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
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RESULT 3
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: Apo-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
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; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-780-496-1

Query Match      100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYYVFTNKLKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYYVFTNKLKQMDKYSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
Db 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQKVQYIYKTSYPPDILLMKSGARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRQOEIKENTKNDKQKVQYIYKTSYPPDILLMKSGARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 4
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
; US-08-883-086-10

Query Match      100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYYVFTNKLKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYYVFTNKLKQMDKYSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
Db 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKNDKQKVQYIYKTSYPPDILLMKSGARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRQOEIKENTKNDKQKVQYIYKTSYPPDILLMKSGARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 5
US-09-320-424-2
; Sequence 2, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER FILING DATE: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-09-320-424-2

Query Match      100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYYVFTNKLKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYYVFTNKLKQMDKYSKSGIACFLKE 60
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61	Qy	DDSTWDPNDESMNSPCQVQVKWQLRQLVRKMILRTSEETISTVQBKQKQINISPLVRGPQ	120
61	Db	DDSYDPNDESMNSPCQVQVKWQLRQLVRKMILRTSEETISTVQBKQKQINISPLVRGPQ	120
121	Qy	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHRLNGELVIHEKG	180
121	Db	RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHRLNGELVIHEKG	180
181	Qy	FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCSKDAEYGLY	240
181	Db	FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCSKDAEYGLY	240
241	Qy	SIYGGIFELKENDRIFVSVTNEHLIDMDHSPASFFGAFLVG	281
241	Db	SIYGGIFELKENDRIFVSVTNEHLIDMDHSPASFFGAFLVG	281

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RESULT 6
US-09-333-593A-6
; Sequence 6, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333.593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 281
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-333-593A-6

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RESULT 7
US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CNI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-157-864-11

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RESULT 8
US-09-825-563-2
; Sequence 2, Application US/09825563
; Patent No. 6521228


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; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-09-825-563-2

Query Match      100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
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DB 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 10
US-09-582-450-1
; Sequence 1, Application US/09582450
; Patent No. 6740739
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Kelley, Robert F.
; APPLICANT: O'Connell, Mark P.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Schwalli, Ralph H.
; TITLE OF INVENTION: Apo-2 Ligand
; FILE REFERENCE: P0978P4
; CURRENT APPLICATION NUMBER: US/09/582,450
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/007,886
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 09/060,533
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-450-1

Query Match      100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
```

```
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-09-825-563-2

Query Match      100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 9
US-09-919-039-118
; Sequence 118, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
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Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 11
US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. 6746668
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match 100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDNDPNDSESMNSPCQVQWQRLVRLKMLRTSEETISTVOEKQONISPLVRERGPO 120
Db 61 DDSYWDNDPNDSESMNSPCQVQWQRLVRLKMLRTSEETISTVOEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDQMVQYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDQMVQYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 12
US-10-011-125A-4
; Sequence 4, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125A-4

Query Match 100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDNDPNDSESMNSPCQVQWQRLVRLKMLRTSEETISTVOEKQONISPLVRERGPO 120
Db 61 DDSYWDNDPNDSESMNSPCQVQWQRLVRLKMLRTSEETISTVOEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDQMVQYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDQMVQYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 13
PCT-US96-10895-2
; Sequence 2, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

Db 1 MAMVEQGGPSLGGTCLVLIIVFTVLLQSLCAVATYVYPTNELKQMDKYKSGIACFLKE 60
Qy 61 DDSYWDPNDESMNSPCWQVKQLRQLVRLKMLRTSEETISTVQEKQKQNISPLVRERGPQ 120
Db 61 DDSYWDPNDESMNSPCWQVKQLRQLVRLKMLRTSEETISTVQEKQKQNISPLVRERGPQ 120
Qy 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVHEKG 180
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVHEKG 180
Qy 181 FYIYSQTYFRFQEBIKENTKNDKQKVQYIYKTSYPPDPILLMKSARNCSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEBIKENTKNDKQKVQYIYKTSYPPDPILLMKSARNCSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14

US-09-072-993C-3

; Sequence 3, Application US/09072993C

; Patent No. 6346388

; GENERAL INFORMATION:

; APPLICANT: Michael R. Brigham-Burke

; APPLICANT: Peter R. Young

; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND

; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2

; FILE REFERENCE: GH-50030

; CURRENT APPLICATION NUMBER: US/09/072,993C

; CURRENT FILING DATE: 1998-05-06

; PRIOR APPLICATION NUMBER: 60/055,513

; PRIOR FILING DATE: 1997-08-13

; PRIOR APPLICATION NUMBER: 60/056,980

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/057,550

; PRIOR FILING DATE: 1997-08-29

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 279

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-072-993C-3

Query Match 99.3%; Score 279; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 6.6e-277;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVATYVYPTNELKQMDKYKSGIACFLKEDD 62
Db 1 MMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVATYVYPTNELKQMDKYKSGIACFLKEDD 60
Qy 63 SYWDPNDESMNSPCWQVKQLRQLVRLKMLRTSEETISTVQEKQKQNISPLVRERGPQV 122
Db 61 SYWDPNDESMNSPCWQVKQLRQLVRLKMLRTSEETISTVQEKQKQNISPLVRERGPQV 120
Qy 123 AAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVHEKGFY 182
Db 121 AAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVHEKGFY 180
Qy 183 YIYQTYFRFQEBIKENTKNDKQKVQYIYKTSYPPDPILLMKSARNCSKDAEYGLYSI 242
Db 181 YIYQTYFRFQEBIKENTKNDKQKVQYIYKTSYPPDPILLMKSARNCSKDAEYGLYSI 240
Qy 243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279

RESULT 15

US-09-320-424-11

; Sequence 11, Application US/09320424

; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-11

Query Match 66.5%; Score 187; DB 3; Length 253;

Best Local Similarity 100.0%; Pred. No. 6.4e-183;

Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSEETISTVQEKQKQNISPLVRERGPQVAAHITGTRGNTLSSPNSKNEKALGRKINSW 154
Db 67 TSEETISTVQEKQKQNISPLVRERGPQVAAHITGTRGNTLSSPNSKNEKALGRKINSW 126
Qy 155 ESSRSGHSFLNLHLRNGELVHEKGFYIYQTYFRFQEBIKENTKNDKQKVQYIYKYT 214
Db 127 ESSRSGHSFLNLHLRNGELVHEKGFYIYQTYFRFQEBIKENTKNDKQKVQYIYKYT 186
Qy 215 SYDPILLMKSARNCSKDAEYGLYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 274
Db 187 SYDPILLMKSARNCSKDAEYGLYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 246
Qy 275 FGAFLVG 281
Db 247 FGAFLVG 253

RESULT 16

US-09-825-563-11

; Sequence 11, Application US/09825563

; Patent No. 6521228

; GENERAL INFORMATION:

; APPLICANT: Wiley, Steven R.

; APPLICANT: Goodwin, Raymond G.

; TITLE OF INVENTION: Cytokine that Induces Apoptosis

; FILE REFERENCE: 2835-E

; CURRENT APPLICATION NUMBER: US/09/825,563

; CURRENT FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: 09/320,424

; PRIOR FILING DATE: 1999-05-26

; PRIOR APPLICATION NUMBER: 09/190,046

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: 09/048,641

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 08/670,354

; PRIOR FILING DATE: 1996-06-25

; PRIOR APPLICATION NUMBER: 08/548,368

; PRIOR FILING DATE: 1995-11-01

; PRIOR APPLICATION NUMBER: 08/496,632

; PRIOR FILING DATE: 1995-06-29

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11

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; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-825-563-11

Query Match      66.5%; Score 187; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.4e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSETISTVQEKQKQISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 154
Db 67 TSETISTVQEKQKQISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 126

Qy 155 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYT 214
Db 127 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYT 186

Qy 215 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 187 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246

Qy 275 FGAFVLG 281
Db 247 FGAFVLG 253

RESULT 17
US-09-320-424-13
; Sequence 13, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER FILING DATE: 1998-11-10
; EARLIER FILING DATE: 1998-11-10
; EARLIER FILING DATE: 1998-03-26
; EARLIER FILING DATE: 1996-06-25
; EARLIER FILING DATE: 1995-11-01
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-13

Query Match      66.5%; Score 187; DB 3; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.5e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSETISTVQEKQKQISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 154
Db 70 TSETISTVQEKQKQISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 129

Qy 155 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYT 214
Db 130 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYT 189

Qy 215 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 190 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249

Qy 275 FGAFVLG 281
Db 247 FGAFVLG 253

US-09-320-424-13

Query Match      66.5%; Score 187; DB 3; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.5e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSETISTVQEKQKQISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 154
Db 70 TSETISTVQEKQKQISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 129

Qy 155 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYT 214
Db 130 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYT 189

Qy 215 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 190 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249

Qy 275 FGAFVLG 281
Db 247 FGAFVLG 253

US-09-320-424-13
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Db 250 FGAFVLG 256

RESULT 18
US-09-825-563-13
; Sequence 13, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-825-563-13

Query Match      66.5%; Score 187; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.5e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSETISTVQEKQKQISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 154
Db 70 TSETISTVQEKQKQISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 129

Qy 155 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYT 214
Db 130 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYT 189

Qy 215 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 190 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249

Qy 275 FGAFVLG 281
Db 250 FGAFVLG 256

US-09-825-563-13

RESULT 19
US-09-105-343A-7
; Sequence 7, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

RESULT 26
US-09-825-563-4
; Sequence 4, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
US-09-825-563-4

Query Match 32.0%; Score 90; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.9e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

RESULT 27
PCT-US96-10895-4
; Sequence 4, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
```

```
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-4

Query Match 32.0%; Score 90; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.9e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

RESULT 28
US-09-569-611C-32
; Sequence 32, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-32

Query Match 32.0%; Score 90; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.5e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 25 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLQMDKYSGIACFLKE 84
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
DB 85 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 114
```

```
RESULT 29
US-09-569-611C-31
; Sequence 31, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-31

Query Match      32.0%; Score 90; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 4.6e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 60
Db 25 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 84

QY 61 DDSYWDPNDEESMNSPCWQVKQLRLVRK 90
Db 85 DDSYWDPNDEESMNSPCWQVKQLRLVRK 114

RESULT 30
US-09-632-287A-12
; Sequence 12, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422e1 Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/3550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-632-287A-12

Query Match      30.2%; Score 85; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 4.3e-79;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 ERGPORVAHITGTRSNITLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV 175
Db 1 ERGPORVAHITGTRSNITLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV 60

QY 176 IHEKGFYIYSQTYFRFQEEIKENT 200
Db 61 IHEKGFYIYSQTYFRFQEEIKENT 85

RESULT 31
US-09-621-976-6479
; Sequence 6479, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6479
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 27
; OTHER INFORMATION: Xaa = Glu,Gln
; NAME/KEY: UNSURE
; LOCATION: 34
; OTHER INFORMATION: Xaa = Glu,Val
; NAME/KEY: UNSURE
; LOCATION: 33,57
; OTHER INFORMATION: Xaa = Leu,Pro
; NAME/KEY: UNSURE
; LOCATION: 25,32
; OTHER INFORMATION: Xaa = Leu,Val
US-09-621-976-6479

Query Match      8.5%; Score 24; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 6.9e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTV 24
Db 1 MAMMEVQGGPSLGQTCVLIVIFTV 24

RESULT 32
US-09-628-665-14
; Sequence 14, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628,665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771e1 Sequence
US-09-628-665-14

Query Match      5.3%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 RFOEEIKENTKNDKQ 205
Db 1 RFOEEIKENTKNDKQ 15

RESULT 33
US-09-628-665-32
; Sequence 32, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
```


APPLICANT: Greene, Mark I.
APPLICANT: Murali, Ramachandran
APPLICANT: Kinoshita, Masahiko
TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
FILE REFERENCE: UPN3831
CURRENT APPLICATION NUMBER: US/09/628,665
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146,094
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-32

Query Match 5.3%; Score 15; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 RFQEEIKENTKNDKQ 205
Db 3 RFQEEIKENTKNDKQ 17

RESULT 34
US-09-105-343A-8
Sequence 8, Application US/09105343A
Patent No. 6207642
GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-6050
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
FILING DATE: 12-FEB-1998
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/02859
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6048.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
TELEFAX: 847-938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 183 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6207642e
US-09-105-343A-8

Query Match 5.0%; Score 14; DB 3; Length 183;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKTSYDPPI 220
Db 109 VQYIYKTSYDPPI 122

RESULT 35
US-08-670-354-6
Sequence 6, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-354-6

Query Match 5.0%; Score 14; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKTSYDPPI 220
Db 217 VQYIYKTSYDPPI 230

RESULT 36
US-09-320-424-6
Sequence 6, Application US/09320424
Patent No. 6284236
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.

; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 291
; TYPE: PRT
; ORGANISM: murine
US-09-320-424-6

Query Match 5.0%; Score 14; DB 3; Length 291;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKYSYDPPI 220
DB 217 VQYIYKYSYDPPI 230

RESULT 37
US-09-825-563-6
; Sequence 6, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 291
; TYPE: PRT
; ORGANISM: murine
US-09-825-563-6

Query Match 5.0%; Score 14; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKYSYDPPI 220
DB 217 VQYIYKYSYDPPI 230

,RESULT 38

PCT-US96-10895-6
; Sequence 6, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10895-6

Query Match 5.0%; Score 14; DB 5; Length 291;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKYSYDPPI 220
DB 217 VQYIYKYSYDPPI 230

RESULT 39
US-09-632-287A-13
; Sequence 13, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 87

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; TYPE: PRT
; ORGANISM: Mouse
US-09-632-287A-13

Query Match      4.3%; Score 12; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 YIYSQTYFRFQE 194
DB 65 YIYSQTYFRFQE 76

RESULT 40
US-09-902-540-14513
; Sequence 14513, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14513
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14513

Query Match      2.8%; Score 8; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 VAAHITGT 129
DB 4 VAAHITGT 11

RESULT 41
US-07-972-481-2
; Sequence 2, Application US/07972481
; Patent No. 5578453
; GENERAL INFORMATION:
; APPLICANT: McDONALD, PETER J
; APPLICANT: JOHNSON, ALAN M
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TOXOPLASMA ANTIGENS AND
; TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 GATEHOUSE ROAD
; CITY: FALLS CHURCH
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,481
; FILING DATE: 12-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: INTERNATIONAL PCT/AU91/00347
; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 446-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-972-481-2

Query Match      2.5%; Score 7; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FOEEIKE 198
DB 2 FOEEIKE 8

RESULT 42
US-09-513-999C-5589
; Sequence 5589, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5589
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 116
; OTHER INFORMATION: Xaa=Ala or Asp or Glu
US-09-513-999C-5589

Query Match      2.5%; Score 7; DB 4; Length 132;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199
DB 9 QEEIKEN 15

RESULT 43
US-09-513-999C-5590
; Sequence 5590, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
```

; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 590
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 116
; OTHER INFORMATION: Xaa=Ala or Asp or Glu
US-09-513-999C-5590

Query Match 2.5%; Score 7; DB 4; Length 132;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199
Db 9 QEEIKEN 15

RESULT 44

US-09-513-999C-5591
; Sequence 5591, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 591
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 116
; OTHER INFORMATION: Xaa=Ala or Asp or Glu
US-09-513-999C-5591

Query Match 2.5%; Score 7; DB 4; Length 132;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199
Db 9 QEEIKEN 15

RESULT 45

US-09-134-001C-5649
; Sequence 5649, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5649
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5649

Query Match 2.5%; Score 7; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ASFFGAF 278
Db 105 ASFFGAF 111

RESULT 46

US-09-096-724B-8
; Sequence 8, Application US/09096724B
; Patent No. 6548290
; GENERAL INFORMATION:
; APPLICANT: McGarry, Thomas J.
; APPLICANT: Kroll, Kristen
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Geminin Gene and Protein
; FILE REFERENCE: 0725.1055-001
; CURRENT APPLICATION NUMBER: US/09/096,724B
; CURRENT FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/085,371
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: human
US-09-096-724B-8

Query Match 2.5%; Score 7; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199
Db 9 QEEIKEN 15

RESULT 47

US-09-096-724B-24
; Sequence 24, Application US/09096724B
; Patent No. 6548290
; GENERAL INFORMATION:
; APPLICANT: McGarry, Thomas J.
; APPLICANT: Kroll, Kristen
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Geminin Gene and Protein
; FILE REFERENCE: 0725.1055-001
; CURRENT APPLICATION NUMBER: US/09/096,724B
; CURRENT FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/085,371
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 209
; TYPE: PRT
; ORGANISM: human
US-09-096-724B-24

Query Match 2.5%; Score 7; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35447
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35447

Query Match          2.5%; Score 7; DB 4; Length 384;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      114 VRERGPQ 120
      |||||
Db      56 VRERGPQ 62

RESULT 51
US-09-270-767-50664
; Sequence 50664, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50664
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50664

Query Match          2.5%; Score 7; DB 4; Length 384;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      114 VRERGPQ 120
      |||||
Db      56 VRERGPQ 62

RESULT 52
US-09-302-626B-186
; Sequence 186, Application US/09302626B
; Patent No. 6709660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizzi, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 186
; LENGTH: 400
; TYPE: PRT

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ORF114a
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (105)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (139)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (179)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (209)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (344)..(355)
; OTHER INFORMATION: place-holder
US-09-302-626B-186

Query Match 2.5%; Score 7; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129
|||||
Db 322 AAHITGT 328

RESULT 53

US-09-198-452A-189
; Sequence 189, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 189
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-189

Query Match 2.5%; Score 7; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSRGH 161
|||||
Db 248 ESSRSRGH 254

RESULT 54

US-09-438-185A-173
; Sequence 173, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPrn0171
US-09-438-185A-173

Query Match 2.5%; Score 7; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSRGH 161
|||||
Db 251 ESSRSRGH 257

RESULT 55

US-09-248-796A-18251
; Sequence 18251, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18251
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18251

Query Match 2.5%; Score 7; DB 4; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SLGQTCV 17
|||||
Db 285 SLGQTCV 291

RESULT 56

US-08-909-125-6
; Sequence 6, Application US/08909125
; Patent No. 6495737
; GENERAL INFORMATION:
; APPLICANT: KLESSIG, DANIEL
; APPLICANT: GUO, AILAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMPROVING
; TITLE OF INVENTION: SALICYLIC ACID-INDEPENDENT SYSTEMIC ACQUIRED DISEASE RESISTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA

; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,125
; FILING DATE: 11-AUG-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,033
; FILING DATE: 12-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: JANET E. REED, PH.D.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-563-4100
; TELEFAX: 215-563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 554 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-909-125-6

Query Match 2.5%; Score 7; DB 4; Length 554;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 KALGRKI 151
Db 477 KALGRKI 483

RESULT 57
US-09-302-626B-183
; Sequence 183, Application US/09302626B
; Patent No. 6709660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 183
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ORF114a
; NAME/KEY: SITE
; LOCATION: (47)..(73)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (85)

; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (296)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (343)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (352)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (377)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (417)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (447)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (582)..(593)
; OTHER INFORMATION: place-holder
; US-09-302-626B-183

Query Match 2.5%; Score 7; DB 4; Length 628;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHTGT 129
Db 560 AAHTGT 566

RESULT 58

US-09-949-016-11022
; Sequence 11022, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11022
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11022

Query Match 2.5%; Score 7; DB 4; Length 645;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TVLQSL 29
Db 278 TVLQSL 284

RESULT 59

US-09-831-642-34
; Sequence 34, Application US/09831642
; Patent No. 6635751
; GENERAL INFORMATION:
; APPLICANT: HAZE, Kiyosuke et al.

RESULT 61
US-09-302-626B-179
; Sequence 179, Application US/09302636B
; Patent No. 6709660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido

; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 1574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ORF114-1
US-09-302-626B-179

Query Match 2.5%; Score 7; DB 4; Length 1574;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129
Db 560 AAHITGT 566
|||||

RESULT 62
US-09-302-626B-60
; Sequence 60, Application US/09302626B
; Patent No. 6709660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 1978
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-302-626B-60

Query Match 2.5%; Score 7; DB 4; Length 1978;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129
Db 560 AAHITGT 566
|||||

RESULT 63
US-09-415-522-6
; Sequence 6, Application US/09415522A
; Patent No. 6291660
; GENERAL INFORMATION:
; APPLICANT: Gaffney, Thomas
; APPLICANT: Wendland, Juergen
; APPLICANT: Philippsen, Peter
; TITLE OF INVENTION: Development
; FILE REFERENCE: CGC2046
; CURRENT APPLICATION NUMBER: US/09/415,522A
; CURRENT FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6
; LENGTH: 2071
; TYPE: PRT
; ORGANISM: Ashbya gossypii
US-09-415-522-6

Query Match 2.5%; Score 7; DB 3; Length 2071;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 SSPNSKN 143
Db 48 SSPNSKN 54
|||||

RESULT 64
US-09-628-665-13
; Sequence 13, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinosaki, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628,665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-13

Query Match 2.1%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 SRSGHS 162
Db 1 SRSGHS 6
|||||

RESULT 65
US-09-628-665-31
; Sequence 31, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinosaki, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628,665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-31

Query Match 2.1%; Score 6; DB 4; Length 10;


```
;
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6348328e
US-08-858-207A-268

Query Match          2.1%; Score 6; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 FTNELK 43
Db 19 FTNELK 24

RESULT 70
US-09-270-767-42298
; Sequence 42298, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42298
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42298

Query Match          2.1%; Score 6; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TGRSN 134
Db 29 TGRSN 34

RESULT 71
US-09-328-352-6548
; Sequence 6548, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6548
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6548

Query Match          2.1%; Score 6; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 IACFLK 59
Db 1 IACFLK 6

RESULT 72
US-09-513-999C-7381
; Sequence 7381, Application US/09513999C
; Patent No. 6783961
```

```
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7381
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 31
; OTHER INFORMATION: Xaa=Glu or Lys
US-09-513-999C-7381

Query Match          2.1%; Score 6; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 SNLHLR 170
Db 25 SNLHLR 30

RESULT 73
US-09-270-767-32209
; Sequence 32209, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32209
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32209

Query Match          2.1%; Score 6; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 AEYGLY 240
Db 25 AEYGLY 30

RESULT 74
US-09-248-796A-27194
; Sequence 27194, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
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; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27194
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-27194

Query Match 2.1%; Score 6; DB 4; Length 76;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 VLLQSL 29
Db 36 VLLQSL 41

RESULT 75
US-09-107-532A-5502
; Sequence 5502, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5502:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...78
; SEQUENCE DESCRIPTION: SEQ ID NO: 5502:
US-09-107-532A-5502

Query Match 2.1%; Score 6; DB 4; Length 78;
Best Local Similarity 100.0%; Pred.No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 NDESM 73

Db 21 NDESM 26

Search completed: June 22, 2005, 06:53:25
Job time : 45 secs